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THE 81st ANNUAL MEETING OF THE ASSOCIATION OF SOUTHEASTERN BIOLOGISTS

~Cancelled by the COVID-19 Pandemic~

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SOUTHEASTERN BIOLOGY

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PURPOSE

The purpose of this association shall be to promote the advancement of biology as a science by encouraging research, the imparting of knowledge, the application of knowledge to the solution of biological problems, and the preservation of biological resources. The ASB has representation in Section G Committee of the AAAS. Varying types of membership are available to individuals and institutions. See inside back cover.

TIME AND PLACE OF FUTURE MEETINGS

2021 March 24-27 Chattanooga, Tennessee
2022 Little Rock, AR
2023 Winston-Salem, NC

The View from Here

A MESSAGE FROM THE PRESIDENT
J. CHRISTOPHER HAVRAN, ASB PRESIDENT 2019-2021

Dear ASB Community,

I'm composing this message in May 2020 at my home in Holly Springs, North Carolina. Like many of you I have been working away from my home institution over the past several months to help slow the spread of SARS-CoV-2. As you're aware, the Executive Committee of the ASB voted to cancel our annual meeting that would have taken place in Jacksonville, FL from March 24-28. This was the first time an ASB meeting was not held since 1945, when the meeting was cancelled for several years due to WWII. The decision to cancel was not made lightly, and I think it is in the best interests of the current and future membership to describe the timeline of events that led to the cancellation of the annual meeting.

In late 2019 the SARS-CoV-2 virus was first documented in China and at some later point was transported to the United States and the rest of the world. In February of 2020 the organizers of large scientific meetings became aware of their role in serving as superspreading events and began to cancel their conferences. At first we did not think that a regional meeting like ASB would be impacted like larger, international meetings. We reached out to our members to know that we would be following CDC recommendations at the meeting and were closely monitoring the Florida Department of Health's Website.

In the first week of March the true scope of the virus presented itself and many institutions began to restrict student and employee travel to prevent the contraction and spread of the virus. We received emails from student and faculty members who had already registered for the conference to let us know that their institutions would not allow travel. Several members also notified us that they would not be travelling to the conference to prevent contracting the virus themselves and suggested that we cancel the meeting. We realized in early March that we would likely not be able to hold our annual meeting as planned. On March 11, the early registration deadline for the conference and the same day that the World Health Organization declared the virus a global pandemic, the EC unanimously voted via email to cancel the annual meeting.

The EC discussed the possibility of holding a virtual meeting in the spring. The cancellation of the meeting coincided with the weeks that institutions of higher education moved their instruction to online and sent students home. At this time faculty were in the process of reformatting their courses while students were distributing all over the country to their homes. The ASB also lacked an existing platform to hold a virtual meeting and we were only a few weeks out from our scheduled meeting date. We therefore did not have the same opportunity to explore virtual options that other associations with later meetings had. Because of all of these factors, we decided that we would not attempt to convert the 2020 meeting to a virtual format.

Though we did not provide a venue for the presentation of oral and poster presentations, we are publishing all accepted abstracts in this issue of Southeastern Biology. All accepted abstracts will also remain accessible on our 2020 meeting webpage. For those of you that want or need to list your abstract in a CV, we hope you cite this bulletin, and mention in the citation that the meeting was cancelled due to the 2020 pandemic.

During the days leading up to the meeting cancellation, I spoke frequently with our plenary speaker, Dr. Saundra McGuire. She would have given our plenary lecture and two workshops on the first morning of the conference. Dr. McGuire was incredibly understanding and offered to participate in an electronic plenary. She also allowed her contract to be cancelled without any additional stipulations.

In the weeks leading up to the annual meeting, ASB committees were working hard to review applications and nominations for a variety of ASB-sponsored awards. These awards would have been presented during the Friday evening Awards Banquet. To recognize the accomplishments of our members, we decided to hold a virtual awards banquet on Facebook and Instagram. Committee chairs recorded videos to announce award winners for various ASB support, research, and career awards. Jeremy Barfield compiled and edited all videos. Kim Hays, ASB Archivist and Social Media Manager, posted the videos during the week of May

11-15. For those awards that involved registration reimbursement at the annual meeting, we decided that we would apply those reimbursements to the 2021 meeting in Chattanooga, TN. All other awards would be mailed to award recipients.

Our meeting planner, Shannon Oliphant-Gordan deserves a significant amount of credit for the role she played in the cancellation of the meeting. Shannon puts a tremendous amount of work into planning our meeting every year. When it became obvious that the meeting would need to be cancelled, Shannon managed registration reimbursements and cancellation of all contracted events that would have been held at the conference. She also communicated with the hotel over several weeks, eventually resulting in our release from our meeting contract. We would not have been able to navigate this situation without her experience and guidance.

Cancelling the 2020 meeting was the right thing to do, but we are naturally disappointed that we could not share with you everything that we had been working on over the past few years. Our plenary speaker, Dr. McGuire, was going to contribute more than any other speaker in recent history by providing two workshops on applying metacognition in teaching and learning in addition to her welcoming plenary. We had also just approved our Meeting Code of Conduct. This outlines expected behavior for the annual meeting and details consequences of violations. We hope that having this Code of Conduct in place will make our meetings safer and more inclusive. The ASB community had submitted a large number of workshops and symposia compared to previous years. We had looked forward to providing a venue for all of these events. Finally, we know that hundreds of faculty and students were looking forward to the opportunity to present research at the meeting. They had been working hard on these projects for months or years, and we are always proud to give them a forum to present. We're disappointed we could not achieve that this year.

The past few months have presented unique challenges to all of us. The cancellation of our meeting was a big challenge, but it was made out of the necessity to help maintain the health and safety of our communities. I applaud all of the many efforts you have been taking to protect your own communities while also maintaining your research and education into the Biological Sciences.

The future may be uncertain, but the ASB is committed to holding our full 2021 Annual Meeting, including poster and oral presentations, next year. In case travel restrictions and gathering limits have not reached pre-pandemic levels, we are investigating if and how to hold a blended meeting that would still allow people to present their research. We look forward to providing a venue for you to present your research next year and beyond.

I hope you are all safe and healthy, and I look forward to seeing you next year at the 82nd meeting of the Association of Southeastern Biologists,

J. Christopher Havran
May 11, 2020

ASB 2020 R.H. Martin Plenary Speaker

Dr. Saudra McGuire

Saundra Yancy McGuire, Director Emerita of the LSU Center for Academic Success and Retired Assistant Vice Chancellor and Professor of Chemistry, is an internationally recognized chemical educator, author and lecturer who has traveled the globe promoting sure-fire strategies to help students, including those underrepresented in science and math professions, to be successful in their coursework and careers.

Metacognition: The Key to Improved Learning

Dr. McGuire has travelled the globe promoting sure-fire strategies to help students, including those underrepresented in science and math professions, to be successful in their coursework and careers. In this presentation, Dr. McGuire will discuss her research applying cognitive science based strategies to help learners of all ages experience meaningful, transferable learning.

About the R.H. Martin Plenary

Robert H. Martin, founder and owner of Martin Microscope Company from 1946 until his death in 2006, was an avid supporter of ASB and of the sciences in general. He supported ASB for decades as a Patron member and sponsor of the ASB Student Research Award, and, with his passing, his family established what has become the Robert H. Martin Plenary Address fund to help cover the costs of bringing in highly qualified speakers for the ASB annual meeting.

Featured Institutions

Jacksonville University
University of North Florida

Exhibitors

American Society for Microbiology
Appalachian State University Department of Biology
Associated Microscope, Inc.
Augusta University
Beta Beta Beta
Batelle / NEON
Campbell University College of Pharmacy & Health Sciences
Capital Microscope Services, Inc.
Clear Field Optics
Eagle Hill Institute
Eastern Kentucky University
Georgia Southern University
Jacksonville University Marine Science Research Institute
James Madison University
Martin Microscope Company
National Association of Biology Teachers
PhbeaD
Prescott College
Southern Appalachian Botanical Society
SimBio
University of Louisiana at Monroe
University of North Florida
Winthrop University

Symposia

Informal natural history education: Short exposure, lasting impacts
Organizer: Cindy Bennington, Stetson University, DeLand, FL

This symposium brings together science educators who work outside the traditional classroom to develop and implement short, impactful learning experiences. Speakers bring expertise from nature centers, field stations, museums, botanical gardens, and universities. This symposium would be of interest to science educators, university faculty engaged in the scholarship of teaching and learning, and graduate and undergraduate students who may be considering careers in informal science education.

A CURE for your Curriculum: Implementing Course-embedded Undergraduate Research (CUREs) into your Curriculum
Organizers: Judy Awong-Taylor, Clay Runck, Allison D'Costa and Cindy Achat-Mendes, Georgia Gwinnett College, Lawrenceville, GA

How effective are Course-embedded Undergraduate Research Experiences (CUREs)? There is a growing body of evidence that shows a link between student research and lasting learning, and that research experiences increase students' interest in careers in STEM (National Research Council 2003; Lopatto 2007; Lopatto 2009; Laursen et al. 2010). Lopatto (2007) points out that even a short immersion experience in undergraduate research is enough to effect long-term gains in student motivation for learning, independence, and an understanding of science. These experiences also play a significant role in alumni getting into graduate school, being employed, or both (Schmitz and Havholm 2015). This symposium will provide information and activities on how to implement effective CUREs into the curriculum. The symposium will feature speakers from Georgia Gwinnett College, Clayton State University, Savannah State University, and University of Louisiana at Monroe who have designed and implemented CUREs in biology courses, including introductory biology courses. The symposium will: introduce key components (STEM skills, assessment, etc.) of effective CUREs; include interactive group discussions; and a faculty panel that will discuss successes and challenges to developing and implementing CUREs.

Class Embedded Research: Results, Examples and Practical advice
Organizers: Nathan Reyna, Ouachita Baptist Univeristy, Arkadelphia, AR and Lori Hensley, Jacksonville State University, Jacksonville, AL

This symposium would be a mix of how-to-talks and reporting of scientific data generated using the course-embedded undergraduate research experience (CURE) model. A misconception of the CURE model is these experiences only generate canned or unusable data. Symposium talks will be research-focused but will allow faculty to see how the CURE model can be used to generate real scientific data. Our ideas come from The Cell Biology Education Consortium (CBEC-www.cellbioed.com), an NSF-funded research collaborative network (RCN). Although, the CBEC focuses on CUREs in the context of cell biology, our model is usable across biological disciplines.

Workshops

Increasing Student Motivation: Strategies that Work!
Organizer: Suandra McGuire, LSU Center for Academic Success

This workshop will engage faculty in a discussion of addressing student needs for autonomy, competence, relatedness, self-esteem, and enjoyment in order to significantly increase student motivation.

Making Powerful Research Presentations: A Systematic Metacognitive Approach That Works!
Organizer: Suandra McGuire, LSU Center for Academic Success

This workshop is for students. Have you noticed that some presentations capture your attention and leave you wanting to hear more from the presenter while other make you glad that the talk is finally over? This presentation will provide strategies that will leave your audience in awe of your scientific research and your ability to clearly communicate it with confidence.

Welcome New Colleague: Advice for Early Career Faculty Members at Primarily Undergraduate Teaching Institutions (PUI)
Organizer: Lisa Ann Blankinship, University of North Alabama

The workshop will lead participants primarily through a presentation on "helpful hints" and "best practices" for their early years (years 1-5) at a PUI. Participants will work in small groups (3-5 people) to design one-year, five-year, and ten-year plans, review goals, put together a list of desirable qualities in a colleague mentor, and discuss strategies on how to find colleague mentors. Small group work will be used to facility discussion with group ideas shared with the entire group so that all can learn from each other. Activities: 1) Developing a one year, five year, and ten year plan – Participants will be given time to work on their individual plans before sharing with their small groups (3-5 people). A list of reasonable goals and expectations will be reviewed during the presentation prior to participants working on their plans. Small group participation will allow participants to have help from their peers if they are stuck in a particular area as well as further discuss ideas that they may wish to include in their own plan. 2) Colleague Mentor Discussion – After a brief presentation on the importance of a colleague mentor, participants will work with their small group to develop a list of beneficial quality they would want in a colleague mentor. Small groups will also discuss what traits or qualities they would avoid in a colleague mentor as well as strategies for finding colleague mentors. Ideas from the small group discussions will be shared with the larger workshop group.

Hitting the Ground Running with your Graduate School Applications
Organizer: Veronica Segarra, High Point University

This workshop has been designed to better prepare our undergraduate student members to apply to graduate school. Through dynamic discussion with more experienced ASB member panelists, this workshop will raise participants' awareness of the key elements of successful graduate school applications—especially those that are often not explicitly described to or required from undergraduate applicants. After a short introductory presentation, an interactive moderated discussion will ensue with the help of experienced ASB members who will serve as panelists and answer prepared and real-time participants' follow up questions related to the topic. There will also be short exercises throughout the workshop that will help attendees experience successful strategies for career development. The workshop will end with a short review of the take-home messages to remember.

Strategies for Student Engagement in Biodiversity Collections: A Workshop for the Natural History Organizations for (bio)Diversity and Education (NHODE) Network
Organizers: Kari Harri and Travis Marsico, Arkansas State University

Student involvement in university-based natural history collections can be essential to the survival and proper maintenance of those collections. However, student involvement seems to ebb and flow at many institutions. This workshop explores strategies for and challenges of getting students involved in natural history collections. We will share models that have worked for Arkansas State University and other institutions including starting a Natural History Collections Club (NHCC), providing experiential opportunities

through workshops, and offering formal opportunities through coursework. Our workshop will be divided into two parts. The first hour will be a presentation for those who are not familiar with the Natural History Organizations for (bio)Diversity and Education (NHODE) Network. The second hour will be breakout sessions focused on specific methods of engaging students in biodiversity collections. Participants may attend for one hour or both.

Field Trips

The Nature of Florida's First Coast
Organizer: Natasha Vanderhoff, Jacksonville University

We will visit Guana Tolomato Matanzas National Estuarine Research Reserve (GTMNER-https://gtmnerr.org/) located ~50 minutes south of Jacksonville at 505 Guana River Road, Ponte Vedra Beach, FL 32082, please note GTMNER charges a $3 entry fee. GTMNER's habitat diversity and gradient from the ocean to hammock forest provide a home to hundreds of plant and animal species. Spring is a particularly good time to see migrating birds. Participants will leave hotel at 7:00 AM on Saturday and caravan (Transportation not provided) to GTMNER. Meet in the hotel lobby to caravan. At GTMNER we will meet in the parking lot and hike trails at GTMNER from 8:15 – 11:15, explore wildlife, with particular emphasis on birds and herps. We will then visit the Environmental Education Center after our hike. Lunch is not provided but participants can enjoy some of the local restaurants on their own.

Ordway-Swisher Biological Field Station
Organizer: Andrew Rappe, Ordway-Swisher Biological Station

The field trip will tour the research facilities and observation tower at the University of Florida IFAS Ordway-Swisher Biological Station. We will discuss on-going research projects (including NEON), as well as land management activities such as controlled burning. Visitors will see Longleaf pine Sandhill habitat as well as numerous water bodies. Transportation: Field trip attendees must provide their own transportation. Ordway-Swisher is approximately 1 hr 15 minutes away from the convention center.

ASB Prestigious Awards
Presented Through the Virtual Awards Banquet
May 11-15, 2020

ASB SUPPORT AWARDS

The Lafayette Frederick Underrepresented Minorities Scholarship ($1200)

David Smith, University of Tennessee Chattanooga, Chattanooga, TN

Support Award For Graduate Student Members Of Asb ($250 Plus Asb Banquet Ticket)

Chasity Moore, Winthrop University, Rock Hill, SC
Jesse Sockman, Eastern Kentucky University, Richmond, KY
Jonathan Kilroy, University of Alabama, Tuscaloosa, AL
Katie Krogmeier, Appalachian State University, Boone, NC
Kristin Conrad, Eastern Kentucky University, Richmond, KY
Lauren Pharr, North Carolina State University, Raleigh, NC
Molly Gooden, Western Carolina University, Cullowhee, NC
Nicholas Shieler, Marshall University, Huntington, WV
Rebekah Shupe, Marshall University, Huntington, WV
Shannon Matzke, Georgia Southern University, Statesboro, GA
Tyler Annarino, Marshall University, Huntington, WV

Support Award for First-Generation Undergraduate Student Members of ASB ($250 Plus ASB Banquet Ticket)

Andrea Appleton, Georgia Southern University, Statesboro, GA
Noah Brown, Kennesaw State University, Kennesaw, GA (ESA sponsored)
Elizabeth Cabrera, High Point University, High Point, NC
Amanda Harless, Georgia Gwinnett College, Lawrenceville, GA
Kabryn Mattison, Appalachian State University, Boone, NC
Quaid Pendleberry, Marshall University, Huntington, WV
Victoria Romero, Kennesaw State University, Kennesaw, GA
Sharon Spiess, Abraham Baldwin Agricultural College, Tifton, GA
Aamani Thulluru, Stetson University, DeLand, FL
Gabriella Tyler, Georgia Gwinnett College, Lawrenceville, GA
Danielle Ury, Middle Georgia State University, Macon, GA
Bryce Wetherell, Middle Georgia State University, Macon, GA

ASB RESEARCH AWARDS

ASB Student Research Award ($1000)
Sponsored by Martin Microscope

Steven Gardner, Auburn University, Auburn, AL
Innate immunity of Florida cane toads:
How dispersal has affected physiological responses to LPS

ASB Research Award ($1000)

No award was made this year.

ASB Student Oral and Poster Presentation Awards

Each year, ASB recognizes outstanding student **oral** and **poster presentations** at the annual meeting. These awards are given in **animal biology**, **aquatic biology**, **cell and molecular biology**, and **microbiology**. Each student awardee receives $300. Unfortunately, due to the cancellation of our meeting this year, we were unable to recognize the outstanding work of our student ASB members.

ASB CAREER AWARDS

ASB John Herr Lifetime Achievement Award

No award was made this year.

ASB Meritorious Teaching Award

Jennifer Rhode Ward, University of North Carolina Asheville, Asheville, NC

ASB Lucrecia Herr Outstanding Biology Teacher Award

Dr. Nicole Mossblech, Vero Beach High School, Vero Beach, FL

From top left: Chris Havran (President), Ashley Morris (Past President), Chris Brown (incoming President Elect), Davy Giles (Member-at-Large); Second row, from left: Heather Joesting (incoming Member-at-Large), Kim Hays (Archivist), Matt Heard (Member-at-Large), Tracy Deem (Treasurer); Third row, from left: Ted Zerucha (Member-at-Large), Holly Boettger-Tong (Member-at-Large), Alfredo León (incoming Vice President), Loretta Ovueraye (Secretary); Fourth row, from left: Veronica Segarra (incoming Member-at-Large), Shannon Oliphant-Gordon (Meeting Planner), Jim Caponetti (not pictured; Editor); Not pictured: Chris Gissendanner (Associate Treasurer).

ASB Oral Presentation Abstracts

1 - Urban and rural gray catbird (Dumetella carolinensis) songs elicit different territorial responses

Morgan Rhodes[1], T. Brandt Ryder[2,3], Dana Moseley[1,2]

[1]James Madison University, Harrisonburg, VA, [2]Smithsonian Migratory Bird Center, Washington, DC, [3]Bird Conservancy of the Rockies, Fort Collins, CO

Birdsong is a sexually selected mode of communication used for mate attraction and territory defense. Vocal signals, such as birdsong, are partially masked by low-frequency urban noise, potentially limiting signal transmission. Previous studies demonstrate that urban and rural birdsong differs structurally, specifically in terms of minimum frequency. However, few studies have tested the territorial response of male birds to male song from different habitats along an urban gradient, particularly in vocal mimics. We hypothesized that male gray catbirds (*Dumetella carolinensis*) would respond more aggressively to songs from similar habitat types, as they represent a familiar stimulus. Across an urban gradient from Virginia to Washington D.C., we conducted 32 paired playback experiments, with each focal male receiving urban and rural catbird song stimuli. We measured aggression based on several behavioral markers such as latency to approach the speaker, time spent close to the speaker, and number of flights, songs, and soft songs. Individual male response varied based on habitat between urban and rural song treatments. Rural male catbirds responded more aggressively to rural song, while urban birds responded more to urban song, and suburban birds responded similarly to each. Structural differences between urban and rural catbird song exist, and the results of this experiment suggest these differences may affect the degree of aggressive response. These findings are evidence that songs across an urban gradient may be diverging, as catbirds can distinguish between urban and rural song and modify their aggressive responses accordingly. Songs from similar habitats may convey a higher level of threat than those of dissimilar habitats, as they are more familiar.

2 - The effect of parenting styles and biparental cooperation on reproductive success in the Carolina chickadee (Poecile carolinensis)

Molly Gooden

Western Carolina University, Cullowhee, NC

Socially monogamous birds use biparental care to off-set the high cost of energy, resources, and time needed to successfully rear their offspring. To be effective, biparental care requires cooperation between the parents. While parental effort and task allocation have been well studied in birds, less research has focused on how cooperation between parents affects their reproductive success. In this study, I investigated consistent between-individual differences in parental behavior (i.e. parenting styles) and how parenting styles influence strategies of cooperation in Carolina chickadees. I examined individual effort towards provisioning versus nest defense to understand the variation in parenting styles among chickadee parents. I measured provisioning effort as visits per hour per chick during 8-hour observational periods using a video camera at the nest. I measured nest defense effort as the distance (m) from predator during 7-minute trials using a taxidermic predator near the nest. I estimated similarity between the parents using z-scores of parental behavior and I measured reproductive success as chick growth per day, fledgling mass, and number of chicks fledged. I found a statistically significant positive correlation in effort between provisioning and nest defense in individuals, so parents were either high, medium, or low contributors in their approach towards parental care. Further, I found that parents with similar parenting styles produced good quality chicks. But if pairs were dissimilar, a greater contribution by males produced the higher quality chicks than when males provided little parental contribution. The cause of consistent between-individual differences in parental care remains largely speculative, but the degree of parental contribution provided by the male chickadee in a pair impacts chick quality. The results of this study suggest that male parental contribution in Carolina chickadees is critical when parents are dissimilar in their parental effort.

3 - The Effect of Noise Pollution on Urban Bird Diversity and Abundance at Two Neighborhood Feeders

David Feng, Darlene Panvini

Belmont University, Nashville, TN

Noise pollution refers to the proliferation of sounds from the environment that can negatively impact animal life. Noise pollution varies in urban environments and can affect bird behaviors related to communication and levels of stress. Louder noises were expected to correlate with decreased bird abundance and diversity. Birds were surveyed at two urban neighborhood sites using feeders containing black sunower seeds and millet. The number of bird visits, species, occurrence of male and female cardinals, and intensity of sound were recorded in 2-minute intervals for one hour on consecutive days at each site for six weeks. The louder site experienced greater abundance, the greatest number of bird visits were seen at the intermediate noise levels, there was no noticeable difference between the diversity of the two sites, and there was no correlation between the loudness of sound with diversity and abundance. A confounding factor might have been the length of time the feeders were established pre-observation. Another limiting factor that might have skewed the results was the total number of measurements that were taken at each sound interval as most of the sound measurements that were taken fell within the intermediate noise intensities. Improvements that can be made in the future would be to take an equal number of measurements at each sound intensity (i.e. low, medium, and high) in a controlled environment to get more precise results. Future studies could examine noise and bird occurrences at various urban sites to better preserve urban bird diversity and abundance.

4 - Are Newly Emerged Females of the Polka-Dot Wasp Moth Mute?

Francisco Coro

Miami Dade College, Padrón Campus, Miami, FL

Syntomeida epilais (Erebidae, Arctiinae), known as the polka-dot wasp moth, is one of the few lepidopterans that require acoustic communication for successful mating behavior. Starting normally on their third night after emergence, perched, virgin females respond with their acoustic signals to conspecific male emissions. My aim is to determine if newly emerged females (one and two nights after emersion) are able to respond with their acoustic emissions to the playback of a series of conspecific male emissions and that of an attack sequence from a sympatric bat species. 18 one night old and 22 two night old females were acoustically stimulated while perched during their normal courtship behavior hours, between 3:00 and 6:30 AM. All these 40 females responded with their acoustic signals to the bat attack sequence, while only five of them responded to their male signals. For both stimulation series they showed high threshold, around 90 dB SPL. As control, 18 three night old virgin females were stimulated with the same acoustic signals and under the same conditions. All 18 three night old females responded to their male signals and to the bat echolocation calls, showing a significant decrease in their threshold, between 54 and 60 dB SPL. These and other results show that these female moths with two-celled ears emerge with a fully functional acoustic system (both reception and emission), but that they require a "maturation" of their auditory system of at least three nights to respond to their male signals for successful mating.

5 - The Effect of Anthropogenic Food Sources on Coyote Diets in Urban and Rural Habitats in the Piedmont of South Carolina

Bethany Krug

Winthrop University, Rock Hill, SC

With increasing rates of urban expansion, interactions between humans and wildlife become inevitable. These urban environments present novel situations to native species, frequently resulting in their displacement or extirpation. However, some species, often referred to as "urban adapters", have thrived in these landscapes. Coyotes (*Canis latrans*) are a prime example of a species that has adapted to exploit urban habitats. Coyotes are omnivores with food choices ranging from small/medium mammals to invertebrates depending on habitat. With their recent range expansion into the Southeast, little is known of their behavioral ecology in the region, especially details relating to their diet. Macroscopic and stable isotope analyses of scat were used to study the diets of rural and urban coyotes in the Piedmont Region of South Carolina to assess the relative content of anthropogenic food sources in their diet. Over three time intervals (breeding, 1 January- 30 April; pup-rearing, 1 May-31 August; 1 September- 31 December), 20 scats were collected from 13 sites; 10 scats were urban, and 10 scats were from rural locations. Macroscopic materials were separated into categories of bone, hair, seeds, vegetation, insect exoskeletons, and anthropogenic materials. To identify the presence of anthropogenic food sources that may not have been visible macroscopically, stable isotope analysis was used. Higher $\delta^{13}C$ content is an indication of potential anthropogenic food sources due to corn-based foods being a primary staple of human diet in the region. We hypothesized that urban coyote diets would contain more anthropogenic food sources and thus have higher carbon levels compared to rural diets. We found that there was no significant difference in ^{13}C and ^{15}N isotopes in coyote scats between rural and urban environments overall nor any significant difference in ^{13}C and ^{15}N isotopes between rural and urban habitats across seasons.

6 - Say My Name, Say My Name: Integrating Statistical Methods for Defining Species within Complexes

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Recent studies have highlighted a need for more refined tools in species delimitation. This is especially true when considering diversity within species complexes, where members are morphologically similar and where traditional tools have thus far failed to provide clearly defined boundaries between species. This project seeks to refine our traditional tools of species delimitation and apply new tools to the challenges created by species complexes. The focus organisms of this study are the frogs of the *Limnonectes kuhlii* complex. This species complex comprises more than 25 species of stream frogs from Southeast Asia. Traditionally, morphometrics (particularly linear measures) has been the most common way to demonstrate differences between two or more species. Unfortunately, traditional approaches to morphological analyses placed members of this group into a single, widely distributed species for nearly 200 years. Recent studies combining genetic, morphological, and bioacoustic tools have been effective in delimiting some, but not all potential species. The currently undescribed members of the *L. kuhlii* complex (candidate species) provide an opportunity to investigate new approaches to morphological character analyses (e.g., geometric morphometrics), and to refine traditional approaches (alternative statistical analyses) used in species delimitation. Ultimately, this project aims to recognize, delimit, and describe real biological diversity in order to facilitate conservation efforts aimed at protecting these frogs and the habitats that they live in.

7 - Crowd Mapping: Modeling Species Distributions with Citizen Scientists

J. Brandon Fuller

University of North Carolina, Chapel Hill, NC

A fundamental goal of conservation is to be able to determine what organisms are extant and, of those extant organisms, predicting where they could occur. Conservationists have traditionally relied on long hours in the field meticulously tracking and recording individuals of species and cross-referencing ecosystem and topology maps to determine new locations for said species. This project sought to speed up the process of modeling species distribution by evaluating the use of a species monitoring app (i.e. iNaturalist©) as a stand in for systematic data gathering by trained researchers. iNaturalist allows untrained individuals to capture images, GPS coordinates, identification,

and traits of species and upload the observation to a machine learning database. This study used the software packages QGISv3.1 and MaxEnt to create species distribution models for flowering vascular plants of known ranges and varying ranges of rarity using data only obtained by citizens using the iNaturalist app and bio-climatic maps for the contiguous United States. This study found that data collected from citizens can be used to create accurate species distribution models for plants with large distributions and non-rare statuses. Models created for plants with limited data due to fundamental problems associated with citizen science projects were unreliable or lacked strong support. Citizen science projects are a valuable tool for conservationist to model species distributions within a given range and should be implemented whenever possible. Citizen science projects should also be used in conjunction with more systematic approaches to accurately model the distributions of rarer species. Citizen science apps should be further developed and refined for the purposes of creating species distribution models by implementing strategies suggested by the author.

8 - Assessing hunting pressures and the population status of Preuss's red colobus, Piliocolobus preussi, and other diurnal primates in the Ebo-Makombe-Ndokbou forest, Cameroon

Ruth Bowers-Sword[1], Joshua Linder[1], Roshna Wunderlich[1], Ekwoge Abwe[2,3], Bethan Morgan[2,3]

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Red Colobus monkeys are among the most endangered groups of primates in Africa with all 17 species threatened with extinction. The Critically Endangered Preuss's red colobus (*Piliocolobus preussi*) is endemic to the forests of southeastern Nigeria and western Cameroon and is threatened by bushmeat hunting and habitat loss. We investigated the population status of and threats to Preuss's red colobus in an understudied portion of its range - the Ndokbou forest of the Ebo-Makombe-Ndokbou forest block of Cameroon. Data on primate abundance and hunting and logging signs were collected from October to December, 2019. Forest reconnaissance surveys were conducted within seven 4x4km grids distributed across the Ndokbou forest. Six passive acoustic sensors were also deployed to assess the spatiotemporal patterns of gun hunting. Across 218 km of recce surveys, Preuss's red colobus was found to be exceptionally rare in the Ndokbou forest, with one of the lowest primate encounter frequencies (0.005grps/km). *Cercopithecus* species, especially the putty-nosed monkey, had the highest overall encounter frequency (0.27 grps/km), particularly in the most heavily hunted and logged areas. Overall, we observed that the least logged areas exhibited the highest overall primate abundance. We conclude that logging and hunting have nearly extirpated red colobus monkeys from the Ndokbou forest and that they may now be confined only to the most mountainous, difficult to access parts of the forest.

9 - Amphibian Species Richness as a Potential Indicator of Wetland Condition in Eastern Kentucky

Jacob L. Stark, Stephen C. Richter

Eastern Kentucky University, Richmond, KY

Wetlands are important ecosystems, providing many ecological and economic services. Despite their importance, over 80% of wetlands in Kentucky have been destroyed. Intensive wetland assessment techniques are necessary for informed management and conservation to take place. However, direct measurement of anthropogenic impact on wetland condition is difficult. Many amphibians rely on wetlands for breeding, larval development, and as habitat space and can be used as indicators of wetland condition. Previous sampling efforts in central Kentucky indicated a positive relationship between amphibian species richness and wetland condition as measured by the Kentucky Wetland Rapid Assessment Method (KY-WRAM). As part of an effort to establish metrics for an Amphibian Index of Biological Integrity (IBI) that reflects wetland condition across the state, we studied amphibian communities in eastern Kentucky. We collected amphibian species richness and abundance data, littoral zone slope, canopy closure, and water quality measures in twenty-five wetlands across a disturbance gradient on the Western Allegheny Plateau. Amphibian data were compared to environmental variables and KY-WRAM scores to determine the relation of amphibians to wetland conditions. Initial analyses revealed a positive relationship between species richness and wetland condition. Analyses of community composition and abundance will be presented to further clarify this relationship. This effort will advance the process of establishing metrics for use in the Amphibian IBI, including species richness, average coefficient of conservatism (C-value), the proportion of sensitive species, and the proportion of tolerant species at a wetland. These metrics will later be combined in the IBI and tested against an independent disturbance index for use as an intensive wetland assessment tool.

10 - Predicting the Effect of Habitat Loss on Heterozygosity in a Small Population: Null Model Approach

Erin Scott, Kevin Smith

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Habitat loss affects ecosystems globally, leading to biodiversity loss, including species and genetic diversity loss. Based on the number of individuals lost, a rarefaction model assuming random circumstances can be used to help predict species loss. The loss of genetic diversity, however, is more complicated to predict. Decrease in allelic richness, one metric of genetic diversity, can be predicted using rarefaction, because it is sample-size dependent. Another metric of genetic diversity, expected heterozygosity (H_e), known to be a good predictor of population fitness, is widely accepted to be sample-size *insensitive*, due to the assumption that rare alleles are unlikely to be lost in a large population. Assuming this, a habitat before and after a disturbance event should retain the same H_e. I expect that this *will not* hold true when a population is very small (i.e., near extinction) and that H_e decrease in a small population can be modelled under random assumptions. In this study I will combine genetic analysis with a simulation analysis I am developing to explicitly test the population-size-sensitivity of H_e, using an experimental population of butterfly milkweed, *Asclepias tuberosa*. After documenting the genetic diversity of the plant population at six microsatellite loci, I then simulate a sudden reduction in population size of the plant population using a custom R script designed to calculate the magnitude change in H_e based on population reduction of different magnitudes. Running this simulation with different percentages removed will allow me to determine whether H_e is size dependent in small populations, and, if so, at what percentage loss we expect decrease in H_e to occur. Given the known importance of genetic diversity to conservation of small populations, an improved understanding of how ecological disturbance, population size, and genetic diversity are interrelated can contribute

to more informed conservation decisions regarding small, endangered populations.

11 - Multi-Marker Meta-Barcoding of Appalachian Karst Cave Eukaryotic Microbes

Bruce Cahoon, Robert VanGundy

The University of Virginia's College at Wise, Wise, VA

Caves are known to harbor assemblages of microbes (microbiomes) but their abundance and identifications are difficult to ascertain. Meta-barcoding surveys of cave prokaryotes have revealed that a small percentage of those on speleothems (cave formations) and about half of those in cave sediments are found in nearby surface soils. This has challenged the assumption that most cave microbes are surface-dwelling organisms that are routinely introduced into sub-surface ecosystems by water, air-flow, or biological vectors. Instead, it appears that cave adapted microbes primarily inhabit those ecosystems, and are perhaps endemic species. Caves are known to harbor eukaryotic microbes but these organisms have received less attention. The purpose of this study was to survey the eukaryotic microbiome of karst caves to address the following question: Is the eukaryotic microbiome of these cave systems comprised of cave adapted endemic species? Water samples were collected from six caves located in the Appalachian region of Southwestern Virginia, DNA extracted from the microbes that were present, and two barcode markers (18S V4 rDNA and 23S rDNA) were PCR amplified and sequenced. 48 unique eukaryotic microbe Amplicon Sequence Variants (ASV's) were identified with the 18S barcode, the majority of these (31) were Alveolates. One group of Alveolates, the apicomplexans, stood out since only cave specific ASVs were recovered. For the 23S barcode, 73 ASVs were identified and the majority (44) were raphid or Nitzschioid diatoms. Among these, several Cryptophytes and Chlamydomonads were recovered as potential cave endemics. These results suggest that some groups of eukaryotic microbes in caves, e.g. diatoms, are indeed introduced from the surface while others, alveolates and heterotrophic algae, may be endemic.

12 - Fishing for New Antimicrobials: Synergism between Fatty Acids and Piscidin Treatment

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A promising avenue for discovery of therapeutic agents involves studying host defense molecules produced by all known species on Earth: antimicrobial peptides. These members of the innate immune response, by virtue of structure and charge, destabilize biological membranes and potentiate killing of bacteria, viruses, fungi and yeast. The first antimicrobial peptides isolated from vertebrate mast cells were the fish piscidins P1 and P3, whose contrasting antibacterial activities involve Cu^{2+} binding. Other recent reports have uncovered the varied effects of exogenous polyunsaturated fatty acids (PUFAs) on bacteria, inducing changes in membrane permeability and altering resistance to antimicrobials that target membrane dynamics. The current study explores the activity of P1 and P3 against *Vibrio cholerae* independently and in combination with fatty acid supplementation. To accomplish this, we assessed membrane permeability and antibiotic resistance in fatty acid-exposed *V. cholerae* treated with P1 and P3. Using four physiologically relevant fatty acids (linoleic, arachidonic, eicosapentaenoic, and docosahexaenoic acids), we observed significant decreases in membrane permeability following fatty acid exposure. When P1 and P3 were administered, their antimicrobial effectiveness was changed depending upon fatty acid supplied in the media. The MICs of P1 and P1Cu were decreased when 18:2 and 22:6 were available and increased when 20:4 was present. The influence of fatty acid exposed *V. cholerae* depended on the Cu^{2+} binding status of P3. Subinhibitory P1 and P3 were also applied for measuring their impact on membrane permeability in the absence of PUFAs. Taken together, our results defined the antibacterial effects of two piscidins on *V. cholerae*. Furthermore, we observed synergistic *and* antagonistic piscidin susceptibility patterns elicited by dual treatment with exogenous PUFAs. The findings further highlight the potential for cationic antimicrobial peptides as therapeutic agents, as well as the intriguing possibility that PUFAs can augment bactericidal activity.

13 - Assessing the threat posed by antibiotic resistant bacteria in an urban river

Matthew Heard, Chris Barton, Rachel Hongo

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The emergence of antibiotic resistant bacteria in urban rivers poses a significant threat to ecosystem and human health. However, in most urban rivers, we lack an understanding of how common resistance is, how this threat changes spatially and temporally, and how bacterial genetic diversity effects the emergence of resistance. In this study, we aimed to address these issues by examining how antibiotic resistance varied in a common fecal indicator organism – *Escherichia coli* (*E. coli*) – across the Cumberland River in Nashville, TN over a two-month period in 2019. To carry this out, we collected 160 water samples from eight locations along the Cumberland River in January and February and assessed these samples for the presence of *E. coli*. Using samples that tested positive for *E. coli*, we determined whether isolates showed resistance to eight common antibiotics: (Chloramphenicol (30 µg), Erythromycin (15 µg), Kanamycin (30 µg), Neomycin (30 µg), Novobiocin (30 µg), Penicillin (10 units), Streptomycin (10 µg), and Tetracycline (30 µg). Furthermore, we used phylogrouping to determine whether different isolates of *E. coli* varied in resistance levels to different antibiotics. Across our sampling effort, we found 140 isolates of *Escherichia coli* and we determined that 100% of isolates were resistant to at least five types of antibiotics. We also found no significant differences in the mean number of colony forming units of *E. coli* between our two sampling times. However, we did find that the presence of *E. coli* and the types of antibiotics that isolates showed resistance to varied depending on where the samples were collected and depending on what phylogroup the isolate was from. Ultimately, our findings suggest that the emergence antibiotic resistant bacteria may pose a growing threat in the Cumberland River and that more information is needed to determine the causal factors driving these trends.

14 - Isolation and identification of anaerobic bacteria in decayed teeth

Jeniffer Lacayo

Georgia Gwinnett College, Lawrenceville, GA

The oral cavity is an excellent habitat for a wide range of bacteria of which a significant proportion are facultative or strict anaerobes. Traditional phylogenetic methods suggest that there are over 700 distinct species in the oral cavity; however only 280 have been cultivated and characterized in the laboratory. Sizova, M. V. et al. estimated that less than half of bacterial species-level taxa from the oral cavity can be cultivated under anaerobic conditions. These microorganisms can contribute to serious disease including dental caries.

Dental caries cause a destructive condition of the dental hard tissues that can progress to inflammation and death of vital inner pulp tissue. If untreated it may lead to the eventual spread of infection to the periapical area of the tooth and beyond. The organisms involved are often located in deep crevasses of the oral cavity such as periodontal pockets and ligaments and can thrive in these low oxygen environments. The goal of this project is to isolate and identify novel anaerobic microorganisms in decayed teeth. Nineteen different isolates were cultured after selection for anaerobes. These were characterized biochemically and phylogenetically. Several of these were identified as medically important species commonly found in diseased oral microbiomes. A potentially novel bacteria related to the proteobacteria, *Microbulbis sp.* was isolated as well as three previously uncultured stains of anaerobic bacteria.

15 - The antimicrobial activity of N,N'-bis-substituted triazolium salts

Julie Wilson, Kerri Shelton, Lauren King

Columbus State University, Columbus, GA

Bacterial infections pose a significant threat to immunocompromised patients, particularly those who are undergoing chemotherapy. This prompts the development of cancer therapeutics that also exhibit effective antimicrobial activities. Increasing multi-drug resistance (MDR) in multiple bacterial species, specifically ESKAPE pathogens, increase the importance of these therapeutic alternatives, as traditional antibacterial treatments are proving to be ineffective or dangerous to patient health. In this study, we examined the bacteriostatic and bactericidal effects of a series of triazolium salt derivatives with a collection of representative bacterial pathogens including *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Enterococcus faecium*, and an MDR clinical isolate of *Acinetobacter baumannii*. We characterized bacteriostatic and bactericidal effects of the derivatives as well as their cytotoxicity. All derivatives exhibited variable activity against pathogens, with compounds containing the 1,2,3-triazole parent having a stronger bacteriostatic effect than those containing the 1,2,4-triazole or benzotriazole parent. Furthermore, derivatives containing the 1,2,3-triazole parent consistently exhibited bactericidal effects against all pathogens except *A. baumannii* while the remainder varied based on the attached substituents. Overall, the methylnaphthyl substituent appears to be a significant moiety that warrants further investigation as it maintains the strongest bacteriostatic and bactericidal effects against pathogens across all parents. Further studies must be done to elucidate the value of these alternative treatments, but the results suggest that ESKAPE pathogen susceptibility to triazolium salt derivatives may result in novel therapeutics to prevent these infections in immunocompromised patients.

16 - Pledged Land Gift to be Transformed Into Biodiversity Center in Bibb County, AL

Joan Rundles

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In April of 2019, Mr. William D. Hubbard made a generous donation of 2,017 acres of his land in Bibb County, Alabama to The University of West Alabama (UWA). The property is approximately 55 miles southwest of Birmingham. Upon his death the property, with 4 miles of frontage on the Cahaba River, will be deeded to UWA for its use and to share with other educational entities. As such, the property has been named the Cahaba Biodiversity Center, for the study of biodiversity, conservation, environmental education and research. Mr. Hubbard's desire is for the property to be conserved for future generations. Furthermore, he wishes for the property to be used right away for educating others about the importance of conservation and environmental education.

The property includes numerous valuable habitats, leading to rich biodiversity. Found there are riparian areas, calcareous woods, and limestone glades, for example. Around half of the property is composed of cultivated timber. A botanical inventory is already in progress, including the location of one federally threatened species, *Arabis georgiana*. In addition, *Croton alabamensis*, an Alabama endemic, grows abundantly on the property. The species collected have been vouchered and deposited in the UWAL herbarium curated at UWA.

17 - The Vascular Plant Flora of Cherokee County, Georgia

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In Georgia the county represents a refined geographical unit for tracking plant distributions: although only the twenty-fourth largest state in area, Georgia (154,007 km^2) has the second highest number of counties (159), for an average of 969 km^2 per county. The focus of this paper is Cherokee County, the fifty-first largest county in Georgia (1,137 km^2, located in the north-central part of the state). The county is a potential center of biodiversity due in part to the effects of three ecoregions: the Piedmont, Blue Ridge, and Ridge & Valley. Based on the digitized voucher specimens at GA and REH Herbaria and others available via the SERNEC portal, the goals of this study were to: (1) transcribe GA Herbarium specimen label data for Cherokee County; (2) review supplementary collections records from the other voucher sources to compile a preliminary species list; (3) conduct a series of collecting trips targeting localities with potential new county records; and (4) georeference and plot all specimens from the county. A legacy checklist for the county, based on vouchers at 14 herbaria and com-

prising 472 species, was generated to serve as a baseline at the onset of the project. Georeferencing these historic specimens revealed that collection efforts had been concentrated in in the northwest and northeast portions of the county and a central-southwest zone. For this study, 284 additional specimens were collected from April of 2017 to September of 2019 at nine targeted sites chosen to supplement historic collecting gaps. These collections included 160 new records for the county, resulting in a final tally of 632 species now vouchered for Cherokee County. Thirteen percent of the flora is exotic. Seventeen species are listed as rare in Georgia, and state protection status has been conferred on *Cypripedium acaule*, *C. parviflorum*, *Schisandra glabra*, and *Xerophyllum asphodeloides*.

18 - Signature of floristic change and an alien invasion in the herbarium record for Lancaster County, Pennsylvania

Kevin Faccenda, Christopher Hardy

Millersville University, Millersville, PA

Situated near major urban population centers in the eastern United States and having the serendipity of being the historical long and short-term residences of many prominent botanists, the vascular flora of Lancaster County, Pennsylvania has been the subject of targeted botanical exploration since 1780 and is thus considered one of the more well-known floras in North America. Yet our analysis of more than 27,000 digitized herbarium records from more than 90 herbaria revealed new country records for 151 species. This represents a surprising 9% increase in the known flora of a county that had been the subject of more than two centuries of botanical exploration. These discoveries are a testament to the efforts over the last decade to digitize herbarium collections and to make them available on the Web. When one delves deeper into the herbarium record and looks at the assembly of the Lancaster Flora through time, however, unsettling evidence is found that the flora is changing in ways that could have long-lasting ecological and economic impacts. While the relationship between the accumulation of native species through time is asymptotic, for example, the accumulation of new alien species is not. While the majority (74%) of the county flora is native, there is a significant trend towards the present of an increasing majority of new county records being alien species.

19 - Enabling automated herbarium sheet image post-processing through neural network models for color reference chart detection

Dakila Ledesma, Caleb Powell, Joey Shaw, Hong Qin

University of Tennessee at Chattanooga, Chattanooga, TN

The digitization of natural history records, such as herbarium specimens, is generating a large dataset with many unexplored novel applications. Concerted efforts of curators, researchers, and volunteers has made millions of Plantae records, with associated images available on open portals such as iDigbio and SERNEC. The digitization of these specimens is heavily dependent on manual processes, such as the white balancing orientation correction of images. Additionally, many of the manual post-processing corrections necessary to make these available are performed on batches of images rather than individual images, which may result in consistency issues between images within each batch. Automation of these processes using neural networks and algorithms may alleviate these problems and expedite the availability of digitized specimens to public databases. It may also enable other features not commonly done for the post-processing of images, such as the determination of scale (e.g. automatic determination of mm/pixel). We present the results of the creation and use of novel neural networks as well as other algorithms for automatic white balancing, orientation correction, and scale determination of digitized herbarium specimen images. Through this presentation, we hope to further incentivize, inspire, and develop future collaborations in the ever-important intersection of Botany and Data Science.

20 - Saxifraga tridactylites (Saxifragaceae) Naturalized in the Southeastern and Northwestern United States

Courtney Alley[1], Erica Rylander[1], Jacob Dawson[2], Mary Feely[1], Dakila Ledesma[1], Nate Parrish[1], Caleb Powell[1], John Shelton[1], Wayne Barger[3], Paul Davison[4], Joey Shaw[1]

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Saxifraga tridactylites (Saxifragaceae), an annual herb native to northwest Africa, southwestern Asia, Europe, northeastern Iran, and western Russia has rapidly naturalized in two geographically distinct areas of the United States: the Southeast and the Northwest. The species' preference for exposed and rocky limestone habitat makes it a significant threat to native species of the Interior Low Plateau and Ridge and Valley provinces where limestone and calcareous glades and woodlands are located. Prior to our work, *S. tridactylites* appeared to be an insignificant introduction, only documented in a few North American locations in British Columbia and Oregon; but the spread of this species has been exceedingly fast in the Southeast, with records from 53 counties collected over the span of seven years. Here, we present a timeline of the introduction and spread of *S. tridactylites* in the Southeast and discuss the threat its increased distribution could have on the rare or endangered glade species of the Southeast.

21 - Credentialing and Careers in the Bioscience Industry

Tamara Mandell

University of Florida, Alachua, FL

The Biotechnician Assistant Credentialing Exam and Bioscience Industry Careers

Biotility, the education and training arm of the University of Florida's Center of Excellence for Regenerative Health Biotechnology (UF CERHB) was established to enhance Florida's competitive ability to attract and grow a world class biotechnology industry; building on the availability of responsive and relevant education and training programs which provide a multi-tiered source of workforce talent.

The *Biotechnician Assistant Credentialing Exam* (BACE) was established in 2012 at Biotility to support economic development and provide skilled workers for Florida's expanding Biotechnology Industry. The opportunity to earn industry-recognized credentials is becoming increasingly important in programs designed to prepare students for careers, and as a result the BACE is now utilized nationwide.

We invite you to learn about the development of the credentialing exam, the involvement of the bioscience industry for its recognition, and outcomes. We will also discuss strategies for success when preparing for the BACE.

- Learn specifics relating to industry involvement in the development of the BACE, and the positions to which it aligns.
- Discuss Biotechnological/Biomedical Science program content and skills in the context of bioscience industry knowledge and skill sets, as represented on the BACE. Participants will also identify strategies and best practices for success.
- Participate in discussions about the bioscience industry work environment, and career options.

22 - Increasing Student Learning and Motivation: Implementation of Specifications Grading in a Sophomore Level Undergraduate Cell Biology Classroom

Shoshana Katzman, Jennell Talley, Elisabeth Javazon, Alessandra Barrera, Jennifer Hurst-Kennedy, Mary Diaz, Mary Beth Anzovino

Georgia Gwinnett College, Lawrenceville, GA

Assessments used in specifications grading have shown to be beneficial for student learning and motivation compared to traditional grading systems. We implemented specifications grading in Cell Biology, creating 20 unique learning outcomes (LOs), where each is assessed by a LO quiz. Mastery of the material on each quiz is the basis for the final grade that the student earns in the course. If students were unable to master the content on their initial attempt, they could earn re-takes for each LO assessment by completing an assignment associated with the information covered in that LO. The ability to re-take assessments is a strategy used in specs grading to increase student effort and give the student more control over their grade. Initial analysis of student attitudes towards specifications grading shift towards positive responses as compared to traditionally graded sections.

23 - An Integrated Introductory CURE for Sophomores Increases Research Interest, REU Applications, & Academic Success

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Course-based undergraduate research experiences (CUREs) have positive effects on student learning, retention in science, and understanding of research. In addition, we report an increase in post-CURE research participation. A small proportion of CUREs in biology are interdisciplinary or at the introductory level. Our CURE fills those gaps by integrating the laboratory components of O-Chem and Intro Biology; students spend 6-7 hours per week with drug design, synthesis, and testing of potential biofilm inhibitors. CURE students are compared to students in a control with a traditional "cookbook" lab experience (CBLE). Instructors and all course materials are identical for CURE and CBLE cohorts; only the laboratory experiences differ. CURE students perform better overall, and the number of students leaving science is reduced (by 45 % for Biology and 93 % for Chemistry). Student responses reveal that the increased academic success may result from understanding the relevance of the material to "real world" applications. An impressive outcome is the large numbers of students that gain an understanding of authentic research and build confidence in their own abilities. Two to 4.5 times more students in CURE versus CBLE participate in post-CURE undergraduate research. Student responses also indicate that over 90 % of the participating students gained an understanding of the discovery and applied natures of research, as well as the authentic frustrations present in research. The first two renditions of this CURE had small cohorts (23-27) while the last two renditions were double in size to test scale. Initial analyses indicate the scaled-up version will afford the same successes. In the future, transferability will be tested. Finally, in 4 renditions of the CURE 400+ compounds were synthesized and 30+ of these new compounds specifically inhibit biofilm formation in one of the 6 bacterial species tested benefiting the research programs of both instructors.

24 - Introducing Undergraduate Students to Marine Biodiversity Using the REEF Survey System

Michael Renfroe

James Madison University, Harrisonburg, VA

In an annual field study conducted in the waters surrounding St. Croix, USVI, students are introduced to marine species identification and classification by categorical frequency based on the Reef Environmental Education Foundation (REEF) criteria. Students are introduced to underwater photographic documentation and species disambiguation. Student-generated data provide a basis for discussions about evolutionary adaptations and survival strategies. This activity provides a longitudinal database for snapshot observations regarding changes in biodiversity at six reef locations around the island. In addition to using species counts as a measure of biodiversity, students use categorical data to explore concepts of community ecology and behavioral adaptations. The REEF survey system is a simple sampling method that effectively can be used to introduce students to marine aquatic biodiversity.

25 - Novices and Nerds: Data validity in the study of birds

Bill Ensign

Kennesaw State University, Kennesaw, GA

Increased interest in Course-Based Undergraduate Research Experiences (CUREs) has led many faculty to incorporate CUREs into their classroom. A perceived advantage of using CUREs is that they allow faculty to leverage their limited time, effort, and resources by combining teaching and research into a single experience. Ideally, data gets collected, students learn by doing, and over the course of multiple iterations the faculty member gets a publication. For these benefits to be fully realized the validity of the data generated by students needs to be equivalent to that of any other well-constructed scientific investigation. To assess the quality of student generated data, I designed a 4-week lab module where students (novices) used a well-defined protocol to collect presence/absence data on bird species at four fixed stations around a lake on the Kennesaw State University campus. During the same period of time, an expert (the nerd) also collected data using the same protocols at the same stations. Novice and nerd data were compared in two ways. First, species accumulation curves and asymptotic species richness for each location were generated for both data sets to assess the reliability of novice data for studies of bird community composition. Second, detection probabilities of selected species for both data sets were estimated to assess novice data reliability for studies of bird species ecology. Results indicated that asymptotic species richness was similar for both data sets, but the nerd rate of species accumulation was much more rapid. Detection probabilities of visible, vocal species were similar between novices and nerds but detection probabilities of smaller, cryptic species were much lower for novices. These results suggest that execution of a well-designed pilot study with potential to reveal inconsistencies in data between novice and expert researchers is essential to successful implementation of CUREs in field-based studies.

26 - The effect of floral textures on the foraging of naïve hawk moths

Benjamin Allen, Amanda Grimes, Joaquin Goyret

The University of Tennessee at Martin, Martin, TN

Manduca sexta are large, nocturnal hawk moths that feed on nectar by hovering steadily in front of a flower and repeatedly tapping the flower's surface with their long, thin proboscis. This probing is an exploratory behavior done to gather information about the surface of the flower, ultimately leading them to the nectar reservoir. Upon tactile detection of floral features such as grooves, *M. sexta* frequently display a Back-and-Forth (BnF) movement in which they orient themselves parallel to the groove and run their proboscis through the groove. Thus, we are able to associate the presence of this conspicuous BnF motion to the detection of a grooved surface. We use 3D printed discs with grooves of decreasing width (1.0 , 0.1, 0.05 mm, and smooth) as surrogate flowers in order to estimate the mechanoreceptive spatial sensitivity of the proboscis. Results indicate moths can detect grooves as small as 0.1 mm, while further trials are being carried out to determine if they can detect even smaller 0.05 mm-grooves.

27 - Comparison of COI Variants in Birds from Urbanized and Natural Habitats

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Genetic diversity has been known to be negatively correlated to urban development because population decline leads to biodiversity loss. Comparison of genetic diversity between locations that have a variety of degrees of urbanization can express to biologists the changes in a population's genetic health. Urbanization's affect towards avian population's nucleotide and haplotype diversity was analyzed to document biotic homogenization. Avian body feathers were collected from three locations in Gwinnett County, Georgia. Harbins Park displays a 95% natural habitat, while Georgia Gwinnett College and Collin Hill Park shows a 50% natural habitat. The collected species include House Wren, American Robin, American Goldfinch, and Field Sparrow which are known facultative migrants that migrate minor distances or stay in Georgia year-round. The mitochondrial gene cytochrome c oxidase subunit 1 (COI) was sequenced to measure diversity, and the number of variants in the species are calculated at the three locations. It was hypothesized that avian species in more developed environments result in a lower number of haplotypes along with a lower quantity of haplotypes (alleles) and nucleotide diversity compared to species in less urbanized habitats. Results show that American Goldfinch and American Robin showed more nucleotide diversity in less urbanized habitats than urban habitats, but other species require a larger sample size. In haplotype diversity, American Robin and Field Sparrow show increasing diversity with decreasing urbanization, but remaining species, while not contradicting the hypothesis, require a larger sample size to show comparable results.

28 - A Multi-Approach Investigation to Evaluate Compounds that Mitigate Neuroinflammation

Gabriella Hernandez-Tyler, Cindy Achat-Mendes

Georgia Gwinnett College, Lawrenceville, GA

29 - The Effect of Nest Placement and Temperature on Reproductive Success in the Barn Swallow

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Barn Swallows are obligate insectivores, and with the predicted collapse of insect populations, the implications for Barn Swallow populations necessitates a close look at their behavior and survivorship. For Barn Swallows, coloniality has evolved largely out of necessity due to limited nesting sites. This study was designed to study the effects of coloniality, specifically nest placement, on Barn Swallows'

reproductive success. Data was collected during the breeding season of one colony at Warner Park Nature Center in Nashville, Tennessee. Nests were monitored at least one time per week to determine survivorship, and data was collected on nest temperature, height, and placement on the building within the colony. We hypothesized 1) high nest temperature would be detrimental due to nestlings unable to regulate temperature, 2) increased height would increase survivorship by lowering predation risk, and 3) greater nest density would have a negative effect on reproductive success as risks for predation and disease increased. Results indicated a slight negative relationship between temperature and total nestlings, fledglings, and percent fledged, with correlation coefficients ranging from 0.03 to 0.22. A slight negative correlation was also found concerning nest height with coefficient values ranging 0.03 to 0.53. Nest distance, visibility, and density did not seem to have an effect. Collectively, this study begins to give insights into the effects that limited nest-site selection may have on survivorship of the Barn Swallow, a significant inquiry for understanding the future of the species.

30 - Antipredatory Behavior of Elimia paupercula, Sooty elimia, in response to Faxonius yanahlindus, the Spinywrist crayfish

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Sooty elimia, *Elimia paupercula*, is an endemic freshwater gastropod located in north Alabama. These snails coexist with several snail predators including the Spinywrist crayfish, *Faxionus yanahlindus*. However, little is known about antipredator behavioral responses of Sooty elimia, especially avoidance behaviors to crayfish predators. To examine antipredator behaviors in Sooty elimia, we recorded the average distance snails spent from a source of various predation cues. The cues included chemical cues from the Spinywrist crayfish alone, alarm cues from crushed conspecifics, or a combination of both crayfish and alarm cues. Each alarm cue treatment was compared to a control which contained no cues from predators or conspecifics. Experiments were conducted in the laboratory using 38-L aquaria with three replicates for each of the four treatments. Each experiment was repeated 3 times. Snails were observed and distance recorded relative to the treatment stimulus every hour for 24-hours. A mixed-effects model was used to compare treatments. Distance was used as the response variable and treatment as the explanatory variable. Individual snails, replicate number, and trial period were used as random variables. We concluded that there was a significant effect of treatment stimulus on the snail's average distance. Snails that were exposed to the combined cues of crayfish and crushed snails were on average further away from the stimulus than snails in other treatments. While Sooty elimia displayed predator avoidance behaviors in a laboratory setting, it is still unknown how strong these behaviors would be in natural settings. When snails are exposed to predation cues in a natural stream setting other factors such as stream flow may influence detectability and response to cues by the snails, and as a result the snails' antipredator behaviors.

31 - Stage Based Matrix Modeling of Trifolium stoloniferum Restoration Populations at Taylor Fork Ecological Area, Madison County, Kentucky

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Running buffalo clover, *Trifolium stoloniferum* Muhl. Ex A. Eaton (Fabaceae), is a federally endangered, herbaceous perennial that was once abundant from West Virginia to Kansas and Missouri, but suffered steep decline after European settlement and was once considered extinct. The species is currently pending to be de-listed after extensive recovery efforts. Running buffalo clover reproduces both from seed and clonally, through the rooting of new individuals at the nodes of extended stolons. This species, and many other endangered or threatened plant species, can benefit from more detailed population viability analyses (PVAs) that include information about the size or stage of individuals within populations, rather than just the number of individuals. Stage-based PVAs were conducted for six restoration populations within the Taylor Fork Ecological Area in Madison County, Kentucky, and the results were related to how this type of analysis can and ought to be used in the conservation of this and other endangered species. In order to conduct the analyses, proposed life history stages were first validated, with stolon length being predictive of individual fitness. The stage-based analyses conducted in this project were compared to previous research done with the same restoration populations at Taylor Fork Ecological Area with count-based PVAs to compare the value of stage-based modeling over the simpler count-based methods. Ultimately, even though stage-based modeling is more difficult and consumes more resources, it provides a richer suite of information such as stable stage distributions, reproductive values, and elasticity matrices. This information is valuable to conservation biologists and can be used to more accurately assess a population's status and to focus management activities on life stages that have the most influence on population growth, even when the most important life history stage varies by population, allowing for more efficient and effective management practices.

32 - Virtual reality and serious gaming: The new frontier in environmental education and insect conservation

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Through interactive gaming, virtual reality applied to butterfly and forest conservation activities can reach a broad audience and initiate a paradigm shift towards coexistence between humans and butterflies under urban settings. Butterfly World 1.0 is a serious game designed to teach players about butterflies and plants in dry forest ecosystems. The immersive virtual environment allows players to explore the forest without swarms of mosquitoes and oppressive heat present in the real environment. Rethinking a different way of communicating butterfly conservation and environmental stewardship through gaming, we can reach many who might otherwise remain untouched by traditional education routes. Virtual gaming, designed to educate the player through meaningful tasks and measurable outcomes, presents another avenue for direct knowledge acquisition and passive empathy through direct experiences.

33 - eDNA Surveillance and Genomic Characterization of the Threatened Trispot Darter (Etheostoma trisella)

Kayla Fast[1], Parker Nenstiel[2], Anakela Popp[3], Pat O'Neil[2], Stuart McGregor[2], Brett Albanese[3], Bernard Kuhajda[4], Brook Fluker[5], Michael Sandel[1]

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The Trispot Darter (*Etheostoma trisella*) is a small freshwater fish found in the Coosa River watershed in the southeastern United States. Recently, the trispot darter was listed as a threatened species under the Endangered Species Act (ESA). To describe population genomic diversity in this newly reclassified species, we have inferred evolutionary relationships and gene flow among extant populations using restriction site associated DNA sequencing from Diversity Arrays Technology (DArTSeq). Population genomic analyses for this species include populations from Alabama, Tennessee, and Georgia. In addition to assessing population genomic variation, we are monitoring the distribution of the trispot darter at historical and novel sites. We have implemented an alternative to traditional sampling methods in the form of environmental DNA (eDNA). This type of genetic material is DNA extracted from environmental samples (i.e., water) instead of an individual, biological specimen. We extracted eDNA from filtered water samples and detected the presence of trispot darters using loop-mediated isothermal amplification (LAMP). LAMP detects small quantities of DNA rapidly by amplifying multimeric DNA at a single temperature. Approximately 9,732 single nucleotide polymorphisms (SNPs) were recovered after DArTSeq data were filtered. These SNP data support three genetic populations: one including fish from Ballplay Creek, a second of Little Canoe Creek populations, and a third which includes the Mill Creek, Coosawattee, and Coahulla Creek populations. The data also provide evidence that is concerning for the persistence of these populations. We have confirmed the presence of the trispot darter at some localities where it has historically been found, but were unable to detect their presence at Ballplay Creek. Trispot darter DNA was also detected at additional, possibly novel sites. An understanding of the trispot darter's current distribution, particularly potentially extirpation from historic sites, will provide a platform for conservation efforts and investigation of evolutionary histories.

34 - Quantifying the effects of human trail traffic on wildflower abundance and diversity

Eli Robinson, Benjamin Thornton

Southern Adventist University, Collegedale, TN

Human activities, such as hiking and biking, have been shown to reduce the height, coverage, and species richness of vegetation along trail systems. The goal of this study was to identify to what possible extent these activities along the White Oak Mountain trail system, on the campus of Southern Adventist University, is affecting wildflower population abundance and diversity. Ten permanent quadrants were set up, with variations in elevation and distance from the trail. During the month of April, while wildflower growth is at its peak, data was taken on the variety and abundance of wildflowers in each quadrant. During the same time period trail cameras were placed where they could capture photographs of the quadrant and the adjacent trail, where applicable. The cameras were programed to take a burst of three photographs when motion was detected. By these means, data on human and wildlife traffic at each quadrant were recorded. Data collected in 2015 and 2019 revealed increased trail traffic which did not correlate with effects on wildflower abundance, which significantly increased, or diversity. Diversity was higher in quadrants closer to the trails which may be attributed to increased seed dispersal due to higher traffic through these areas or microecotones.

35 - Introducing a Watershed Scale Stakeholder Engagement Program within the Ecosystem Services Framework to Improve African American Participation in Ecological and Environmental Sciences

Mark Dugo

Mississippi Valley State University, Itta Bena, MS

This presentation introduces an exploratory science education research and watershed monitoring program, funded by the National Science Foundation, to improve stakeholder engagement and increase the participation of African Americans (AAs) in ecological and environmental sciences. The curriculum will combine a citizen science engagement strategy with applied skills in environmental STEM disciplines, using both field and laboratory based research activities. Our place-based framework is designed to characterize watersheds at the basin level and is inclusive of socioeconomic integration. The ecosystem services framework will be utilized to highlight socio-environment interrelations, while concurrently emphasizing the importance of biodiversity and reinforcing cultural connections to the environment. A compliment of activities are proposed including, an undergraduate summer enrichment program, year round environmental monitoring for undergraduate and graduate students, and community outreach. Our curriculum will utilize publically available data sources including, Google Earth Pro, EnviroAtlas, 303d listed streams, TMDL reports, and census data, to identify relevant environmental, social and economic factors necessary for the holistic management of natural resources. Water quality will be correlated to biodiversity metrics obtained through field collections, the use of biological collection databases, and information for species of conservation concern. This project emphasizes the relationship between values, identity, and interest, to foster a deeper connection to the environment among participants. In addition to impacting the STEM environmental workforce, the citizen science component of this project is predicted to empower student participants and proximal communities toward greater social justice and equity, as related to natural resources. Moreover, the current lack of diversity in the ecological and environmental science sectors impede maximal progress for intended environmental protection. By improving AA engagement and participation through a watershed scale - ecosystem services framework, it is predicted that this work will translate to improved ecological conservation and environmental sustainability outcomes at the local and regional scales, minimally.

37 - The effect of Staphylococcus aureus exposure on white-tailed deer trabecular bone stiffness and yield

Emily Long[1], Meir Barak[2], Victoria Frost[1]

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Osteomyelitis is an infection of the bone or bone marrow caused by the infiltration of bacteria, resulting in destructive inflammation, bone necrosis, and abnormal bone remolding. With a growing number of osteomyelitis diagnoses, many of which are linked to *Staphylococcus aureus (S. aureus)*, it is imperative to understand the pathology of *S. aureus* in relation to bone to provide better diagnostics and patient care. While the cellular mechanisms of *S. aureus* and osteomyelitis have been studied, little information exists on the biomechanical effects of such infections. We postulated that exposure to *S. aureus* for 72 hours would significantly decrease both the stiffness and yield of trabecular bone tissue. One hundred and three trabecular cubes (5 x 5 x 5 mm) from the proximal tibiae of *Odocoileus virginianus* (white-tailed deer) were used in this experiment. Bone cubes were sterilized and then swabbed to confirm sterilization before inoculation with *S. aureus*-ATCC-12600 (test group) or sterile nutrient broth (control group) for 72 hours. All cubes were then tested in compression until yield using an Instron 5942 Single-Column machine. Structural stiffness (N/mm) and yield (MPa) were calculated and compared between the two groups. Our results reveal that acute exposure to *S. aureus* does not significantly decrease trabecular bone stiffness or yield.

38 - Proposal of two models of extractive-fermentation bioreactors for the conversion of crude glycerol to biobutanol by Clostridium pasteurianum

Jonathan Kilroy

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Crude glycerol is produced as a major waste product of the bio-diesel industry. Purification of glycerol is difficult and costly due to toxic impurities. The accumulation of crude glycerol hampers the efficiency and economic viability of bio-diesel production, leading to a phenomenon known as the "glycerin glut". Fortunately, the species of bacteria *Clostridium pasteurianum* provides a potential solution. *C. pasteurianum* can rely on glycerol as its sole carbon and energy source while tolerating the toxicities inherent in crude glycerol. This species preferentially converts glycerol into butanol, a useful fuel additive. In order to optimize conversion of glycerol to butanol, a continuous culture chemostat is used to improve cell growth and fermentation via generation of a steady state. The use of an extraction column containing a hollow fiber membrane is explored as a possible method of filtering butanol from the culture. An extraction solution of liposome vesicles is tested and compared to de-ionized water to determine if the addition of vesicles increases the efficiency of the column. Continuous culture of *C. pasteurianum* is found to consistently improve butanol yield over comparable batch cultures while reducing production of minor fermentation products and maintaining exponential cell growth. The extraction column works most efficiently when butanol flow coincides with mechanical volume from the inner tube to the outer shell. The addition of vesicles to the extraction solution does not improve butanol transfer across the membrane. Based on these results, two models are proposed for a bioreactor, one which extracts directly from the culture and one which extracts from the collection vessel. Both models house a continuous culture of *C. pasteurianum* coupled with the extraction column to allow for continuous *in situ* extractive fermentation of crude glycerol into butanol.

39 - Pursuing Pathogens: Examination of Vibrio vulnificus Isolated from Timucuan Preserve, FL

Janel Clarisse Palomo

Jacksonville University, Jacksonville, FL

Vibrio vulnificus are Gram negative marine bacteria that naturally reside in temperate, coastal waters with temperatures greater than 20°C and salinities of 5-25ppt. Virulent strains of *V. vulnificus* have been known to infect individuals who leave wounds exposed or sustain cuts while in coastal waters. The consumption of undercooked or raw shellfish, such as oysters, may also result in infection. Infected individuals may be subject to gastrointestinal distress, severe wound infections, or septicemia. Amputations may be necessary, and death may occur within as little as 1-2 days. In this study, twenty-nine isolates of *V. vulnificus* were obtained from water and oysters of the Timucuan Preserve, Jacksonville, FL, and each was characterized and tested for virulence factors using microbiological and molecular techniques. Water and oyster samples were gathered during mid-tide from the Timucuan Preserve's Sisters Creek over a span of two years, and *V. vulnificus* were isolated on an altered version of highly-selective cellobiose-polymyxin B-colistin agar. Suspected *V. vulnificus* colonies were then identified with matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS), and similarities in the resultant MALDI-TOF MS spectra were utilized to group isolates via dendrogram analysis. *V. vulnificus* isolates were also characterized by Gram stain and fermentation of sucrose and D-cellobiose, sugars often used to differentiate *Vibrio* species. Each isolate's potential for virulence was determined through mannitol fermentation, the presence of a capsule, and hemolytic capabilities. Surprisingly, all Timucuan *V. vulnificus* isolates were capable of fermenting sucrose, a trait not typical of *V. vulnificus*, and 13 of 29 Timucuan isolates displayed D-cellobiose fermentation results that differed from that of *V. vulnificus* controls. In terms of virulence, all Timucuan isolates were capable of fermenting mannitol, and 26 of 29 isolates demonstrated hemolysis. This characterization of *V. vulnificus* contributes to the general understanding of environmental *Vibrio* strains.

40 - Exploring endophytic microbes in pursuit of novel antibiotic synthesis

Emily Rotich, Zaid Hatem, Matthew Heard

Belmont University, Nashville, TN

The Centers for Disease Control and Prevention approximates annual 33,000 deaths caused by antibiotic resistant bacterial infections. There is need to explore naturally produced compounds from endophytic microorganisms for the synthesis of new antibiotics. In this study, we isolated endophytic fungi and bacteria from four plants known for their medicinal values: *Mentha spicata* (spearmint), *Mentha piperita* (peppermint), *Rosmarinus officinalis* (rosemary), and *Ginkgo biloba* (gingko). The surface sterilized cuts from the plants were

cultured in Sabouraud Dextrose Agar; and 86 fungal and 66 bacterial endophytes were isolated. A sample of the isolated bacterial endophytes (22%) were characterized, and then tested for resistance/susceptibility to four antibiotics, Penicillin (P10), Erythromycin (E15), Novobiocin (NB30), and Chloramphenicol (C15). This was done in triplicates. The isolates showed a diverse endophytic population with most of the bacteria being gram-positive bacilli. Over 10% of the isolates were resistant to some antibiotics. This suggests that these endophytic isolates could have natural metabolic products that enable them survive adverse conditions and deleterious compounds. In order to assess whether these antibiotic resistant isolates secreted antibiotic compounds, we studied their interaction with seven clinically relevant bacteria. We observed a zone of clearance on some isolates, and topical overgrowth on other isolates, which suggest possible antibiosis and competition modes of action, mechanisms that need to be explored further.

41 - Establishing an Arboretum on Campus: an All-Encompassing Endeavor

Benjamin Thornton, McKenzie Martin

Southern Adventist University, Collegedale, TN

The process of establishing and maintaining arboretum status on an academic campus provides invaluable opportunities for students, faculty, community members and alumni. Such opportunities include student-led research, horticulture, commemorating loved-ones and academic celebrations, as well as providing an interactive learning tool for the general public. Since 2017, student involvement has led to the tagging, identification, and collection of GPS coordinates of 1,088 trees on campus. Species diversity of the trees on campus has also been calculated. All data has been compiled on our arboretum website, with every tree organized into collections by family, genus and species. Aerial maps of each collection can be viewed on our website allowing users the opportunity to view the location of individual trees on campus from home. Identification plaques have been placed throughout campus for trees within the arboretum collection. These plaques contain QR codes that link them to web-pages that not only describe each tree in detail, but also display diagnostic photographs. Both on our campus and website, special recognition is given to memorial trees and celebration trees. We are currently making our website as user-friendly as possible so that the community can learn more about the trees we have here on campus. Due to the ongoing aspect of this project, future generations can continue to benefit from this endeavor.

42 - Abusing Regular Expressions To Extract Verbatim Coordinates From Herbarium Specimen Labels

Caleb Powell, Joey Shaw

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Natural history digitization has made a staggering amount of specimen images readily accessible. Due to the labor intensive nature of manual data transcription, many of these records are not yet accessible to large scale studies. Label data which has not yet been transcribed is not queryable through the public portals which host them. For example, 58% of *Plantae* specimens hosted through iDigBio are missing the geographic coordinates necessary for geospatial analyses. Although promising, computational technologies such as optical character recognition (OCR) have yet to balance the disparity between specimen images and label data. One challenge such techniques face is accurately classifying textual data into discretized, queryable categories. Here, we will present our efforts to extract geographic coordinates from herbarium specimen labels using OCR and regular expression pattern matching. After failing to solve the OCR classification problem with clever pattern matching algorithms, we resorted to an unreasonably large one which exceeds 130,000 characters. This inelegant method was capable of extracting verbatim coordinates from 10.3% of specimens held in the University of Tennessee at Chattanooga's herbarium (UCHT).

43 - Observations of northern migration in the tropics, an Herbarium and citizen science approach

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Warming temperatures are affecting plant distributions globally. In the northern hemisphere, tropical plant species could move their ranges northward. This northward expansion has previously been documented in several cases, such as the northward expansion of mangrove species along the northeastern coast of Florida. Using herbarium specimens and the citizen science observation platform, iNaturalist, we note tropical plant species that may have recently advanced northward in Florida due to rising temperatures. Anthropogenic-assisted spread through cultivation or inadvertent movement of propagules may be partly responsible. The possibility also exists that these species have long been present but went unnoticed in these areas.

44 - Development of the Herbarium Application for Specimen Auto-Processing, a Real-Time Processing Solution for Herbarium Specimen Images

Caleb Powell[1], Dakila Ledesma[1], Jacob Motley[1], Jason Best[2], Hong Qin[1], Joey Shaw[1]

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Herbarium digitization workflows typically evaluate image capture and image processing as separate, distinct steps. Here we present the ongoing development of a real-time image processing program designed to combine these steps and simplify herbarium digitization. The Herbarium Application for Specimen Auto-Processing (HerbASAP) can perform many procedures common in specimen image processing workflows, including: barcode reading, image orientation correction, white balance, scale determination, blur detection, lens distortion corrections, metadata application, and format conversions. HerbASAP runs concurrently with the image capture step, processing images at a faster rate than most adept imaging technicians. This mode of operation enables real-time image processing and quality control measures without diminishing specimen imaging rates. Here we present on the use of HerbASAP, and describe some of the methodologies

employed by the program.

45 - Virtual Atlas to the Economic Botany Specimens of the James C. Parks Herbarium: a demonstration of strategies and methods of extending the impact of institutional efforts to digitize herbarium records

Christopher Hardy, Emily Ritter, Adam Hummel

Millersville University of Pennsylvania, Millersville, PA

As an important decade in the effort to digitize the world's herbaria draws to close, it is worthwhile to consider strategies for the next decade that might extend the appeal and impact of herbarium holdings to additional user groups other than the usual taxonomists and natural heritage program botanists with taxonomic questions. There is, in fact, a much larger and diverse array of potential users with the thirst for learning more about useful plants, for example, yet who are unaware of the resources offered by herbaria or would find it difficult to navigate the many thousands of specimens and images housed in an institution's herbarium in search of the 1% of the collections that have some notable use for food, fiber, or medicine, for example. We built a virtual portal to the economic specimens in our herbarium in an effort to reach more of our non-taxonomist peers throughout the greater university community. Peers whose primary interests lay with anthropology, for example, might want to know if our herbarium has specimens or artifacts of plants used by particular cultural groups. Peers whose primary interests lay with art might want to search the portal for the names, images and specimens of native fiber plants in the pursuit of an art project using lesser known, alternative fibers. An employee in Human Resources might look for an escape from the world of personnel management for 30 minutes during lunch by surfing a virtual wave of specimen images and dots on the economic portal's interactive map for mangos, aloes and other exotic plants collected in faraway locales. Here we showcase our virtual economic herbarium atlas and discuss the strategies employed in its creation. We hope to further constructive dialogue among botanists who have already created or aspire to create similar tools at their home institutions.

46 - Art as a Gateway to Conservation Science for a Diverse Undergraduate Population

Jenna Palmisano, Justin Pinero, Stephanie Hanson

Stetson University, DeLand, FL

In order to combat the degradation of native Sandhill ecosystems and provide an urban refuge for native flora and fauna, Stetson University faculty and researchers created an urban Sandhill ecosystem restoration site on Stetson's campus in 2011. Since then, undergraduate student interns have been added to the faculty team to assist with the everyday restoration of the landscape. Interns have been tasked with not only the maintenance of the landscape, but with the engagement of the undergraduate community in ways that foster a sense of responsibility for the environment, encourage unconventional interactions with the landscape, and nurture a sense of scientific exploration. With a unique perspective on undergraduate life, the interns have taken an artistic approach to conservation education, crafting and proctoring a diversity of programs and workshops to meet these goals of informal education. Programming has introduced undergraduates to the beauty and ecology of the sandhill landscape through a watercolor workshop, the construction of 3D flowers, citizen science opportunities, and the creation of a tapestry. As the site has matured, the methods by which interns have engaged the student body have evolved. Through this evolution, interns have recognized that events that use abstract methods of engagement through art media attract a larger and more diverse student audience. This still doesn't ensure that these events are inspiring changes in habits and mindsets of students. However, these events do encourage students to slow down and actively perceive the complex natural world, take pride in their unique interpretation of the landscape, and find a new way to engage with nature.

47 - Informal Environmental Education Through Nature Play

Jennifer Hunt

Oakland Nature Preserse, OAKLAND, FL

Unstructured frequent play in informal outdoor settings not only has been shown to boost mental, physical, emotional, and social development in children but can also build a foundation for conservation minded adults. Several factors have influenced the time children spend outside including urbanization, family scheduling, outdoor space availability, among others. Nature Play spaces within urban areas can give children the opportunity to connect with nature close to home.

48 - Creating a Conservation Community

Kristen Marshall Mattson

Spring Island Trust, Okatie, SC

Environmental education programs typically consist of brief exposures to some aspect of natural history but are often limited in that there is not time to adequately establish context of the topic within the bigger picture and the learner may not have background in the topic and therefore cannot scaffold the facts presented with previous knowledge. By creating programs that emphasize hands-on learning and inspire interest and enthusiasm for nature, these limitations can be overcome, increasing the impact of the experience on the individual and the community.

Emphasizing the "experience" part of the learning cycle (experience > learn > apply > repeat) allows all the participants in a program to have a shared background and a starting place from which to build knowledge. In addition, experiential learning ensures participants are exposed to the subject matter in a variety of ways (visual, auditory, kinesthetic, etc.) therefore embracing all learners and increasing understanding of the subject matter.

The impact of environmental education programs increases when the overarching theme of the program focuses on inspiring a positive experience with nature, along with excitement and interest. Given the disconnect many individuals have with the natural world, creating a positive experience is the foundation upon which further interest, questioning, and learning about nature will originate from.

The purpose of environmental education typically relates back to natural resources conservation. By creating programs that emphasize experiential learning and inspire awe of nature, these short experiences can have a lasting impact by creating a community that values conservation through a shared story of the region's natural history along with an appreciation for the environment that will influence decision-making about natural resources.

49 - #MyScienceFuture Project: Promoting nature connections and science careers through art

Dustin Angell

Archbold Biological Station, Venus, FL

#MyScienceFuture is an original arts project that incorporates imaginative play, photography, and drawing into environmental education. Embedded within an ecology summer camp in rural Florida, children study portraits of scientists, dress up for scientist photo shoots, and write messages about their connections to nature and science.

Portraits of summer campers alongside their writing, both created as part a project called #MyScienceFuture. The original art project promotes science careers and expresses the children's connections with nature. This presentation will outline the project and share what it taught his organization about their students.

50 - Hard Mast Production: Collaborations to Standardize Regional Indexing Protocols and Forecast Potential Production Using Forest Inventory

Cathryn Greenberg[1], Chad Keyser[2], Anita Rose[3], Gordon Warburton[4]

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Acorns are important as wildlife food and for oak regeneration. Highly variable acorn production challenges forest managers in gauging crop sizes or estimating yield. Until recently, use of different indexing methods confounded crop comparisons among states. Collaborations between State Agency biologists and US Forest Service researchers lead to a 'toolkit' of methods to simplify and standardize indexing, and tailor acorn production estimates to landscapes. We developed a simple, rapid method to index acorn crop size using visual estimates of the proportion of trees bearing acorns (PBAV) as the independent variable. This replaced labor-intensive, time-consuming acorn crop index methods, and was adopted east-wide by state and federal agencies to standardize indexing for comparable results. Subsequently, we developed models using PBAV to estimate the number of acorns produced within specific years and landscapes, rather than rely on indices. We also used long-term data to develop acorn production capability models based on oak tree dbh, predicted crown area, and average number of acorns per unit crown area. Average production estimates can be tailored to specific stands and different forest management scenarios. Models were implemented into the Forest Vegetation Simulator (FVS-ACORN), the Forest Service's framework for growth and yield modeling. Models allow forest managers to compute average acorn production for their stands through time considering oak decline, mortality, regeneration, and growth, and to analyze trade-offs in forest management alternatives.

51 - Historical fire patterns and the changing importance of xerophytic and pyrophytic tree species within a north Georgia forest.

Christopher Waters, Matthew Weand

Kennesaw State University, Kennesaw, GA

Upland forests within northwest GA were historically dominated by longleaf pine (*Pinus palustris Mill.*) ecosystems. Due to the introduction of fire suppression policies in the early 20th century, longleaf pine systems like these experienced significant declines across the historic range. Today montane longleaf systems are being restored using prescribed fire and historical shifts in species composition and local fire histories are an important consideration for land managers involved in restoration. Consistent with other studies across the southeast, we hypothesized that fire suppression in northwest GA induces mesophication, a compositional shift from historically dominant xerophytic and pyrophytic species to mesophytic and fire-intolerant species. We evaluated this shift by comparing the importance of species in historical land survey maps with modern vegetation surveys. We found a general shift from xerophytic and pyrophytic species such as *Quercus marilandica* Münchh. and *Pinus spp.* L., toward increased dominance of mesophytic and fire-intolerant species including *Acer rubrum* L. and *Oxydendrum arboreum* (L.) DC. Additionally, landscape features such as slope and aspect strongly influenced mesophication with north facing slopes at a more advanced state of mesophication compared to south facing slopes. We also used tree cores to construct a growth chronology for remnant montane longleaf pine stands. The stands we examined primarily persist on south facing slopes as mature canopy dominants with an average stand age of 73.6 years and no evidence of regeneration in the understory. By cross-dating fire scars found in preserved longleaf stumps with the chronology we hope to determine information regarding historical fire frequency. This information can help managers tailor restoration efforts to more effectively restore the montane longleaf system.

52 - Characterization of Seasonal CO2 Fluxes in a Bottomland Hardwood Forest

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Bottomland hardwood forests are alluvial wetlands that occur alongside rivers and streams of the southeastern United States. Flooding is a critical component of forested wetlands with ecosystem productivity and the life cycles of many organisms linked to these hydrological processes, which may also influence carbon sequestration. However, there is a gap in our understanding of the forest-atmosphere exchange of carbon dioxide (CO_2) in these episodically flooded forests. To address this issue, from August 2013 to October 2018, CO_2 fluxes were measured from the top of a 37m tall tower, in a bottomland hardwood forest in northeast Louisiana. This study examines the multi-year seasonal variability of net ecosystem exchange (NEE) of CO_2 and its components, gross primary productivity (GPP) and ecosystem respiration (R_{eco}). For seasonal analysis, the annual cycle of NEE was divided into 3-month periods based on vegetation phenological development and ambient air temperature. The multi-year seasonal NEE averages were 37.79 g C m^2, -35.43 g C m^2, 15.55 g C m^2 and 71.67 g C m^2 for winter, spring, summer and fall, respectively. The forest was a net sink during the spring season (March-May) for each year sampled, indicating a net intake of CO_2 from the atmosphere and conversion into plant biomass. In contrast, during the remaining seasons and on the annual scale, the site was a source of CO_2. The results of this study indicate a strong seasonality and high annual variability in NEE. The seasonal variability was largely attributed to GPP rather than to the R_{eco}. The year to year variability in CO_2 flux was potentially influenced by changes in hydrology. With a characteristic hydrology, bottomland hardwoods will likely be affected by changing climate and land use and it is therefore important to understand the interactions and feedbacks within the carbon cycle.

53 - A spatial and multivariate approach to examining effects of urbanization on nitrogen sources, organic matter inputs, and trophic structure in streams of Cobb and Paulding County, Georgia.

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Land use changes are contributing to a loss of habitat, decreased biodiversity, and loss of stability for ecosystem functions, which can make it more difficult for the stream ecosystem to resist stress and recover following a disturbance (Cardinale and Palmer, 2012). Urbanization has a negative effect on streams often causing a flashier hydrograph and numerous changes in morphology, nutrient concentrations, concentration of pollutants and ecology (Walsh et al., 2005 and Meyer et al., 2005). Biological monitoring is frequently used as an assessment method to detect these effects but adding stable isotope analysis could be valuable because it accounts for temporal integration from anthropogenic wastewater inputs, characterized by a shift in the abundance of ^{15}N. Therefore, the relative amount of ^{15}N found within streams can serve as an indicator and suggest potential solutions to improving stream health by targeting nutrient management. Stable isotopes can also be used to analyze energy flow by constructing food webs within the stream. This study examined spatial trends of $\delta^{15}N$ values across 35 streams with varying levels of urbanization. The lowest Hydropsychidae average $\delta^{15}N$ values were observed in middle and upper Raccoon Creek (5.2 +/- 0.24 and 3.92 +/- 0.15, respectively) and the highest values in Sope creek (10.84 +/- 0.46) and middle Pumpkinvine creek (10.77 +/- 0.74). Based on isotopic signatures, six streams were selected for intensive study to investigate how urbanization affects nitrogen sources, movement of organic matter, and energy transfer through the stream communities to establish a link between stream health and the isotopic indicator. Results of this research will be presented.

54 - Innate immunity of Florida cane toads: how dispersal has affected physiological responses to LPS

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Physiological tradeoffs occur in organisms coping with their environments, which are likely to increase as populations reach peripheries of established ranges. Invasive species offer opportunities to study the types of tradeoffs that occur, with many hypotheses focusing on how immune responses vary during dispersal of invaders. The cane toad (*Rhinella marina*) is a well-known invasive species. Populations near the expanding edge of the Australian invasion have altered immune responses compared to toads from longer established core populations, although this has not been well-documented for the populations in Florida. In this study cane toads from a northern edge (New Port Richey (NPR)) and southern core (Miami) population in Florida were collected and injected with lipopolysaccharide (LPS) to compare immune responses. Physiological differences between the populations included greater metabolic rate increases in LPS-injected toads compared to baseline rates from the core population compared to those from the edge, and higher plasma bacteria killing capability (BKA) in LPS-injected toads from the core vs the edge population. There was also a significant interaction between location and time on circulating corticosterone (CORT) levels following injections with saline or LPS, with CORT decreasing more with time in core population toads. The differential CORT response, which affected timing of circulating leukocyte profile significance and decreased BKA in edge toads, indicates that differential stress responses contribute to the tradeoffs observed with immunity and dispersal.

56 - Why do Photinia leaves infected by Entomosporium mespili exhibit red spots?

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The function of anthocyanins in red halos or spots commonly observed around localized pathogen infections in leaves is not known. We carried out an observational study to document patterns of infection and appearance of red anthocyanin pigments associated with *Entomosporium* leaf spot in red-tipped *Photinia* sp. All expanding leaves appeared bright red, due to high concentrations of five different cyanidin-based anthocyanins concentrated in the leaf mesophyll. Infection by *Entomosporium* occurred exclusively during leaf expansion, and was characterized by appearance of a small necrotic brown spot, on a leaf that was otherwise red. Over the following days to weeks,

leaf tissues around the necrotic tissues remained red, while tissues distal from the infection developed and turned green. In red tissues, chlorophyll content was significantly lower than in green parts of the leaf, and palisade cells were significantly shorter, suggesting delayed development within the red spot. In cases where the leaf successfully contained the pathogen, red halos gradually decreased in size, with red tissues around the necrotic spot maturing into green (from the outside-in); these leaves could subsequently last one year longer or more. However, in other cases, the brown necrosis continued to spread through the leaf, invading red tissues as the lesion increased in diameter; in the most severe cases, the plant prematurely senesced the leaf entirely. From these observations, we conclude that red spots associated with *Entomosporium* infection in *Photinia* are most likely young tissues that have been developmentally "paused", reflecting delayed resource investment in tissues with an uncertain fate.

57 - The influence of environmental parameters on the growth of Thalassia testudinum in a field and laboratory setting

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Thalassia testudinum is a species of seagrass that is ecologically valuable serving as habitat and food for many organisms. Additionally, seagrasses are sediment stabilizers and carbon sinks. There has been a documented decline in seagrass communities over the past decades and in the future, aspects of climate change are predicted to negatively impact seagrass growth. Two broad goals of this study are to understand which environmental parameters may be driving changes seen *Thalassia* communities in the field (Jobos Bay, Aguirre, Puerto Rico) and in the lab to evaluate how different ranges of environmental parameters affect its growth. For the field study, quadrats within established transects in Jobos Bay were resampled. Percent cover, density, and blade height of species within each quadrat were recorded along with environmental parameters.

A PCA was utilized to explore variation in the dataset and visualize relationships between transects and years. A MANOVA was performed to compare whether the linear combinations of dependent variables differed by year and to assess their effect. In the lab, two levels of the variables temperature, pH, and salinity were used to create eight different treatment tanks where *Thalassia* was grown for two weeks and then measured for growth. An ANOVA was performed to determine if growth was significantly different for any treatments.

The PCA analysis showed a trend of increased seagrass cover, canopy height, and seagrass density with a decrease in macroalgae cover and macroalgae Braun-Blanquet from 2017 to 2019. The MANOVA indicated a significant difference between years ($P = 0.014$). Post-hoc tests revealed that pH was the only environmental parameter showing significant difference between years ($P < 0.001$).

The ANOVA on lab data showed no significant differences in *Thalassia* growth for the different treatments investigated ($P = 0.791$ marked growth, $P = 0.934$ new growth).

58 - Quantifying Long-Term HHQ Exposure Using Three Species of Phytoplankton.

Morgan George

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Interactions between phytoplankton and marine bacteria play a vital role in marine food webs as well as oceanic biogeochemical cycles. Previous studies have shown that HHQ, a chemical produced by the bacteria *Pseudoalteromonas picicida*, changed the physiological and growth patterns of a phytoplankton, *Emiliania huxleyi.* Exposure to HHQ resulted in static growth of *E. huxleyi* for an extended period of time. This study will attempt to understand if HHQ has similar effects on three different species of phytoplankton, *Heterosigma akashiwo*, *Thalassiasira weissflogii*, and *Isochrysis galbana*. We found no impact of HHQ on *H. akashiwo* or *T. weisflogii*, but exposure to HHQ resulted in significantly slower growth, higher average red fluorescence, and smaller average forward scatter in *I. galbana*, relative to the controls. As both *I. galbana* and *E. huxleyi* are haptophytes, it may be that HHQ is particularly influential to this Division of phytoplankton. These findings have implications for competition between phytoplankton in the presence of HHQ, and further highlights the importance of bacteria-phytoplankton interactions in the ocean.

59 - Identifying Phenotypic Plasticity of Thermal Tolerance in Endangered Caribbean Coral

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Recent anthropogenic activity has elevated atmospheric CO_2, creating a greenhouse effect that is predicted to elevate global temperatures 1-4° C within the century. Increases in surface temperature pose a threat to the world's coral reefs and have been the cause of many mass bleaching events. Since coral colonies are sessile, survival of individual colonies may require them to acclimate to the increased water temperatures. Phenotypic plasticity, or the ability of an individual to express different phenotypes to survive in different environments, has also been suggested as a critical first step that can buy a population time to evolve important adaptations. This project investigated three questions related to plasticity in high temperature tolerance in endangered Caribbean coral, *Acropora cervicornis*: 1) Are coral colonies capable of acclimating to elevated water temperatures? 2) To what extent are differences in the amount of phenotypic plasticity in thermal tolerance due to differences in coral genotype? 3) Can plasticity be utilized by managers to restore vulnerable reef zones? This study was conducted in two phases. The first utilized a raceway experiment to identify the presence of plasticity in thermal tolerance, as well as estimate broad (H^2) and narrow-sense (h^2) heritability of plasticity of thermal tolerance among *Acropora cervicornis*. The second phase incorporated the transplant of ambient and heat-treated *Acropora cervicornis,* fragments among shallow and deep reef zones in the Florida Keys. The study found that colonies exposed to a previous, short-term heat stress survived a long-term heat stress significantly longer than those that were acclimated at ambient temperatures. The amount of plasticity was found to depend on genotype, but not necessarily to additive effects of genotype. The transplant study suggests depth has a more significant effect upon coral growth and viability than previous heat exposure, but thermal conditioning may still be useful for seasonal warming events.

60 - Monitoring Artificial Reefs in the Gulf of Mexico (GoM)

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Artificial reefs (ARs) are submerged structures used to mimic natural reefs and serve as a biologically diverse artificial ecosystems. Modern artificial reef modules are constructed as one of four main models shapes: quadrilateral, reef ball, cone, and pyramid, and are primarily composed of limestone. A multitude of additional design features have have been added in an attempt to increase the species diversity in communities inhabiting the modules. Such characteristics include increasing topographical complexity, adding holes, crevices, or cracks, and increasing surface area by adding shelves, etc. Aquatic sampling methods developed for the study of fish communities that inhabit ARs include the use of Baited Remote Underwater Video (BRUV) and Underwater Visual Census (UVC) surveys. For this study we sampled existing UVC data made by Mexico Beach Artificial Reef Association (MBARA) to characterize fish community diversity in the Gulf of Mexico (GoM). We analyzed over thirty-six hours of UVC video data in order to establish a randomized sample of video clips. Four MBARA reef locations and a total of eleven AR module types were included in the analysis. All fish present were identified to species and the maximum number of individuals present at any instant during the video clip (MaxN) was determined for each species. Reef areas and module types showed differences in species composition and diversity patterns that reflect primary location differences (reef depth) and AR structural complexity.

61 - Red drum and oyster reef habitat suitability along the Georgia coast to prioritize sites for restoration

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The eastern oyster (*Crassostrea virginica)* and red drum (*Sciaenops ocellatus*) are ecologically and economically important species along the Georgia coast. Georgia's coastal culture, economy, and diet has long been influenced by these species. Throughout the 20th century, overharvesting drove population crashes in both eastern oyster and red drum. The simultaneous effects of overharvesting brood stocks and juvenile habitat (oyster reefs) were particularly devastating. Loss of oyster reefs meant juvenile red drum lost critical nursery grounds and sub-adult individuals had less access to important feeding areas. Recent oyster reef restoration and red drum stock management have led to modest recovery in both populations. We propose that targeted oyster reef restoration of prioritized sites that are ideal for both species (especially in population recruitment life stages) could yield increased returns from management efforts. Our objectives were to create a restoration suitability index by: 1) identifying critical physicochemical parameters and optimal ranges for *C. virginica* and juvenile *S. ocellatus*; 2) create GIS indices that map habitat quality from low to high for both species; 3) combine both indices to produce a dual species habitat suitability index; and 4) modify this index by excluding areas containing potential stressors to either species. Physicochemical habitat suitability indices were created through reclassification of interpolated point water quality data. These data layers were then summed and normalized to create an overall physicochemical habitat suitability index. The index was further modified by incorporating anthropogenic stressors and habitat availability for red drum. Further validation to the model could be achieved by conducting monitoring studies at sites across the habitat quality scale and incorporating red drum population health surveys.

62 - Evolutionary impact of Wolbachia infection among mosquito species

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Inherited bacterial symbionts have played, and are continuing to play, pivotal evolutionary roles in the history of life on earth. One of the most consequential bacterial symbionts in the world currently is an alpha-proteobacterium in the genus *Wolbachia*. Among insects, *Wolbachia* is generally considered a reproductive parasite that manipulates host reproduction to ensure its evolutionary success. The mode of host manipulation has been studied in a large number of host species, and infection phenotypes range from various forms of sex ratio distortion to bacterially induced reproductive isolation. Mosquito species are known to be infected with *Wolbachia* that induce reproductive isolation via a process known as cytoplasmic incompatibility. The evolutionary consequences of Wolbachia-induced cytoplasmic incompatibility are potentially extreme for host insect species, and include effects such as reduced genetic variation and speciation. Mosquito species in the Atlanta metropolitan area were sampled and tested for Wolbachia infection. Phylogenetic analysis of nuclear, mitochondrial, and Wolbachia genes for collected mosquito species suggest several evolutionary effects of infection. Reduced mitochondrial genetic diversity was observed among sampled *Aedes albopictus.* Discordant nuclear-mitochondrial phylogenies among mosquito species was also observed and suggest a possible evolutionary effect of *Wolbachia* infection on patterns of mitochondrial evolution. Statistical analyses of molecular evolution suggest an elevated rate of substitution among certain *Wolbachia*-infected mosquito species.

63 - Testing the Utility of Current Phylogenetic Markers in Genus Neohelix (Gastropoda: Polygyridae)

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Despite their ecological roles as primary consumers and major detritivores, land snails are infrequently prioritized as models of evolutionary change. Consequently, poorly characterized taxonomic relationships are common among polygyrids. Typically, allele variant analysis is employed to elucidate interspecific relationships, however, universal DNA markers have previously produced ambiguous cladistic interpretations among Family Polygyridae. Before taxonomic analysis proceeds, current universal markers must be evaluated for resolution capacity. Genus *Neohelix* (Family Polygyridae) was selected as the model taxon for this study. Instances of homoplasy due to sympatric convergence are common among *Neohelix* species and morphologically similar genera like *Mesodon*, making *Neohelix* a strong candidate for future phylogenetic inquiry. During this study, four genetic loci were PCR amplified with published primers and condi-

tions to assess their utility for identifying polymorphisms: Cytochrome oxidase I (COI), large ribosomal subunits 16S and 28S, and histone 3 (H3). Due to inconsistent amplification, modified COI primers were developed based on polygyrid whole genome reference sequences (KX240084.1 and KX278421.1). Single gene trees were produced, compared to quantify the presence of coalescence or introgression, then concatenated and constructed into a consensus tree. Phylogenetic inference will be discussed as well as implications for *Neohelix* classification.

64 - Patterns of Staminode Evolution in Paronychia (Caryophyllaceae)

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Staminodes are infertile stamens that have evolved numerous times across angiosperms and exhibit a vast array of forms and functions. The variation in staminodial structures and functions suggests complex evolutionary processes underlie their origins, but to understand how and why these processes occur, comparative studies are needed in groups of closely related species. We used *Paronychia* (Caryophyllaceae) as a model system to compare the evolution and development of staminodes across closely related species within a genus. Staminodial structures in *Paronychia* have been referred to as both petals and staminodes, making their identity uncertain. When surveyed across *Paronychia*, structures vary in shape and are absent in some species. We tested the hypotheses that these structures are either petals or staminodes. We evaluated the floral development of fourteen North American species of *Paronychia* with scanning electron and light microscopy and conducted ancestral state estimations across phylogenies to infer when staminodes evolved. Staminodes developed between the outer androecial whorl and the carpel, indicating that they are derived from stamens. In eight species, staminodes developed similar to filaments in shape, length, and time, suggesting that they are vestigial filaments. In four species, staminodes are lost or highly reduced, also suggesting that they are vestigial. In two species, differences in staminode shape compared to filaments suggests functional co-option. A vascular strand was not observed in any species, perhaps indicating that staminodes are vestigial prior to co-option. Staminodes likely evolved before *Paronychia* and were lost at least three times. We argue that staminodes in *Paronychia* began as vestigial structures following the loss of anthers and were either lost, remained vestigial, or coopted. Our results suggest a dynamic history of staminodial evolution in *Paronychia*, and, perhaps, that selection on the function of staminodes is different across closely related species.

65 - The Processing of mRNA's from the Fragmented Chloroplast Genome of Pithophora roettleri

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Species within one green algal order, Cladophorales, have a highly unconventional plastome structure where individual coding regions or small numbers of genes occur as linear single-stranded DNAs that fold to form hairpin structures. This reduced set of genes are primarily required for photosynthesis. Another group of fully photosynthetic organisms with an equivalently reduced chloroplast genome are the peridinin dinoflagellates of the Alveolata eukaryotic lineage. These plastomes are made of mini-circles carrying one or a few genes required for photosynthesis. One unusual aspect of the alveolata is the polyuridylylation of mRNA 3' ends, a phenomenon which has also been observed among non-peridinin dinoflagellates, and the chromerid algae. This study was conducted to understand if an unconventional highly-reduced plastome structure co-occurs with unconventional RNA processing. To address this, the 5' and 3' mRNA termini of the eight known chloroplast genes of the representative species *Pithopohora roettleri* from the green algal order Cladophorales was analyzed for evidence of post-transcriptional processing. Circular Reverse Transcriptase PCR (cRT-PCR) followed by deep sequencing of the amplicons was used to analyze the 5' and 3' termini. Evidence of several processing events was collected, most notably that the 3' termini of six of the eight genes were polyuridylylated, which has not been reported for any lineage outside of the Alveolata. Other processing events include poly(A) and heteropolymeric 3' additions, 5' primary transcript start sites, as well as the presence of circularized RNAs. Other species of green algae, representing different lineages, have also been tested using cRT-PCR and the poly(U) additions appear to be limited to the order Cladophorales which have highly reduced chloroplast genomes.

66 - mRNA Processing of genes encoded on the Mitochondria genome of Pediastrum duplex

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Pediastrum is a freshwater colonial green alga in the family Hydrodictaceae. A *Pediastrum sp.* was isolated from a freshwater river system in Milledgeville, Georgia and cultured. The species was identified as *Pediastrum duplex,* the mitochondrial genome was sequenced and submitted to Genbank (Accession Number MK865949). The purpose of this project was to 1-identify mRNA processing of genes encoded on the mitochondrial genome of *P.duplex*, 2- identify polynucleotide additions during processing events, and 3-explore the possibility that the mRNAs are naturally circularized. The current model for algal mitochondrial processing is that mRNAs are transcribed as one long primary transcript and cleaved into individual genes by exonucleases. These RNAs have long 3' UnTranslated Regions (UTR), but no 5' UTR. The partially processed mRNAs are then either poly-cytidylated, or poly-uridylylated on their 3' termini. mRNAs are then circularized prior to translation; this circularization creates a 5' UTR from the original 3' UTR that initiates translation. In this study, mRNA termini analysis was explored using circular Reverse Transcriptase PCR (cRT-PCR). mRNAs were artificially circularized with T4 RNA ligase and primers were designed to PCR amplify the 3' and 5' UTR junction sites. The process was repeated without artificial circularization and naturally circularized mRNAs were detected. PCR derived amplicons were then deep sequenced using MiSeq technology. Poly-cytidylations were found on linear mRNAs, whereas poly-uridylylations and poly-adenylations were not. Circularized mRNAs lacked poly-cytidylations but contained shorter 3' UTRs and longer 5' UTRs than in other algae. Naturally circularized mRNAs were detected and the junction sites were flanked by specific sequence motifs. This study provides evidence that poly-cytidylations occur on mitochondrial

mRNAs and are most likely unique to the green algae (Chlorophyta). It also demonstrates mRNA circularization among mitochondrial mRNA of green algae.

67 - Phylogenomics, Domestication, and Stable Isotope Analysis of the Invasive Green Swordtail (Xiphophorus hellerii)

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Invasive species are a major factor responsible for the loss of biodiversity, ranking second behind habitat loss. Invasive fishes in particular are an ongoing issue in North America due to their negative environmental and economic impacts. The Green Swordtail (*Xiphophorus hellerii*) is an ornamental fish native to Veracruz, Mexico with a southern range limit extending into Guatemala. They inhabit ponds, rivers, and swift-flowing streams and have been introduced on every continent except Antarctica. To provide insight into the genetic variation, ancestry, and allele frequency divergence of invasive populations, we have sequenced the cytochrome oxidase I (COI) gene of individuals from invasive populations in Florida, Hawaii, Wyoming and Mexico. We have further investigated the domestication of the Green Swordtail using Diversity Arrays Technology (DArTSeq). The single nucleotide polymorphisms (SNPs) generated here strengthen our understanding of the molecular mechanisms that shape the genomes of invasive populations, ultimately leading to successful establishment. By performing stable isotope analysis (SIA), we have also addressed the question of how the Green Swordtail is displacing native fish populations. We used ^{13}C and ^{15}N isotopes to investigate the trophic interactions between the Green Swordtail and native stream fishes. Our stable isotope data show that the Green Swordtail occupies a different trophic niche than the native fishes. Insight into how the Green Swordtail interacts with its community as well as the phylogenetic relationships of native and invasive populations will help improve the understanding of this aquatic invasive species.

68 - Isolating, Purifying, and Investigating Mycobacterial Lysogens

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Bacteria have shared an entangled evolutionary history with bacteriophages (viruses that specifically infect bacteria) for the past three billion years. Some bacteriophages use a specific type of infectious pathway that helps maintain their host's viability and hence enable a mechanism of coexistence.To investigate this further, two temperate mycobacteriophages (ExplosioNervosa and Rhynn) were selected. Both these phages are able to form lysogens and exist in the host cell's genome indefinitely as a prophage. Annotation of their genomes revealed the presence of immunity related genes. These particular genes potentially explain how some bacteriophages are able to protect their host and resist superinfection by other related and non-related bacteriophages. Bacterial lysogens were created by incubating bacterial host cells with the phages. Any resulting mesas were a sign that host cell growth had taken place in the presence of a prophage, so provided a sample of lysogenized bacteria. The lysogens were purified and tested against their original infecting phage as well as an unrelated bacteriophage (Haimas) to see if they were able to resist superinfection. Tests showed that both Haimas and the original viruses were still able to infect the lysogens and cause them to lyse. Infections of these bacteriophages on their own lysogens raised the idea of spontaneous reversion; the prophages could have reverted to the lytic cycle due to a triggering condition in their environment. The ability of the host-phage relationship to respond to certain environmental signals warrants further investigation, as does manipulation of the genes linked with immunity and infection. Investigating the triggers and unraveling the mechanisms that fuel coevolution help further our understanding of the host-parasite equilibrium that exists today and highlights opportunities for future applications.

69 - Identification of Triclosan Resistance Mechanisms in Staphylococcus aureus Isolated from Healthy Carriers

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Triclosan is an antimicrobial agent that, up until its recent ban by the FDA, was a common component of antibacterial consumer products, such as soaps and detergents. Triclosan inhibits fatty acid synthesis, vital to cell membrane formation, by binding to the bacterial enoyl-acyl carrier protein reductase, encoded by the *fabI* gene. Mutations in the *fabI* gene, its promoter and horizontal transfer of the *sh-fabI* gene have been identified in triclosan-resistant clinical isolates. In this study, triclosan resistance was assessed in 297 S. aureus isolates collected from 161 healthy nursing students' noses and throats across three years at the University of North Carolina Wilmington. The isolates were exposed to various concentrations of triclosan on tryptic soy agar plates to determine the minimum inhibitory concentration (MIC) and classify isolates as moderately resistant (MIC ≥ 0.032 µg/mL) or highly resistant (MIC ≥ 0.512 µg/mL). PCR and gel electrophoresis have revealed that many resistant isolates have acquired the *sh-fabI* gene through horizontal gene transfer. PCR amplification and sequencing of the *fabI* gene and its promoter will be used to identify mutations in resistant isolates. The goal is to determine whether mechanisms of triclosan resistance in S. aureus isolated from healthy carriers differ from those in clinical isolates.

70 - Mitochondrial mRNA Fragments are Circularized in a Human HEK Cell Line

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The relatively recent focus on the widespread occurrence and abundance of circular RNAs (circRNA) in the human cell nucleus has sparked an intensive interest in their existence and possible roles in cell gene expression and physiology. The presence of circRNAs in mammalian mitochondria, however, has been under-explored. Mitochondrial mRNAs differ from those produced from nuclear genes because they lack introns and are transcribed as poly-cistronic transcripts that are endonucleolytically cleaved, leaving transcripts with very

small 5' and 3' UTRs. Circular RNAs have been identified in the semi-autonomous organelles of single-celled organisms and plants but their purpose has not been clearly demonstrated. The goal of our project was to test the hypothesis, processed mRNAs are circularized in vertebrate mitochondria as a necessary RNA processing step prior to translation. Mitochondrial mRNAs were isolated from the human cell line HEK293 and evidence of circularization sought by treating RNA with RNAse-R and then amplifying putative 3'-5' junction sites. Sequence results demonstrated the occurrence of mRNA circularization within each coding region of the mitochondrial genome. However, in most cases the circRNAs carried coding regions that had been truncated, suggesting they were not translatable. Quantification of the circularized versions of the mRNAs revealed they comprise a small portion (~10%) of the total mRNA. These findings demonstrate that mRNA circularization occurs in mammalian mitochondria but it does not appear to play a role in making translatable mRNAs.

71 - Should we require all Biology students to take an entire semester of calculus? A former math major and math lover says "NO"!

Howard Neufeld

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Appalachian State University requires all of our majors to take a semester of calculus, a mandate that has been in place for over 40 years, but which has not engendered much serious discussion as to whether or not it makes sense to do this. Herein I argue that few of our majors will ever need to use calculus over the course of their careers (when did your doctor ever require calculus?) and that we should abandon this requirement. We should replace it with a quantitative skills set course that places greater emphasis on the mathematics that students might eventually use, such as arithmetic, algebra and modeling, and couple this with a greater emphasis on statistical analyses, which I suggest all students will need after graduation. Andrew Hacker, professor of mathematics and author of The Math Myth, argues similarly. He exposes the fact that various assumptions about the utility of a mathematical education are just myths, including, for example, the idea that a good grounding in mathematics improves performance in other academic areas. For example, of the 5% of students who scored over 700 on the math portion of the SAT, only 36% of them scored as high in the critical reading section. But of those who scored over 700 on critical reading, 44% scored 700 on the math portion! We should not be basing our curriculum on falsehoods! I propose a revised quantitative skills requirement where students choose between calculus or a mathematics-for-the-life-sciences, coupled with either basic or accelerated statistics, for a total of 7 credit hours of course work. This curriculum would give our Biology majors more flexibility and remove obstacles for students who do poorly in calculus, enabling them to graduate without having their dreams dashed by a requirement that is both cruel and unnecessary.

72 - Thinking Routines, Graphic Organizers, and Guided Journaling on a Short-Term STEM Study Abroad Course

Darlene Panvini

Belmont University, Nashville, TN

Short-term study abroad courses typically span 2-3 weeks and can pose pedagogical challenges for STEM faculty needing to cover a full course of content in a short amount of time. Challenges include: lack of pedagogical resources and research on teaching science abroad; the need to intentionally intervene to structure learning so students have time to process, connect, and reflect to promote deeper thinking; little time for preparation, grading, or content front-loading; and finding balance between class-based instruction and experiential activities. Thinking routines and graphic organizers were incorporated into Guided Journaling Worksheets to address these challenges during a short-term STEM course taught in Costa Rica during a Mayterm. The course, "Conservation and Sustainability in Costa Rica," was developed for both science and non-science majors. The thinking routines and graphic organizers fostered intentional writing that: sharpened student focus, connected experiences with concepts, encouraged thinking and learning, promoted student reflection, and elucidated student concerns. During the trip, the journaling helped students stay attentive to the learning aspects of the trip. The worksheet format of the journal resulted in manageable student and faculty workloads. In addition to study abroad courses, these tools can be a helpful resource for faculty teaching other types of experiential learning courses, including internships, community engagement, field trips, and laboratory activities.

73 - Challenges and opportunities associated with co-advising research students in a classroom setting

Chris Barton, Matthew Heard, Rachel Hongo

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Conducting interdisciplinary research with students can be difficult for faculty without expertise in multiple disciplines. To address this, co-advising of students by multiple faculty members can help students gain experience in disparate fields of study and increase their understanding of how different fields are linked. Here, we present our findings from a semester-long research course that was taught by two science faculty members with different areas of expertise. We highlight the benefits and challenges for students who were co-advised and present the results of surveys that assessed student's understanding of disciplinary techniques and how to conduct interdisciplinary scientific research.

74 - SmokyMtnU: Experiential learning in Great Smoky Mountains National Park

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In Spring 2019, partners at Middle Tennessee State University (MTSU) and Great Smoky Mountains National Park (GRSM) launched a novel experiential learning opportunity dubbed 'SmokyMtnU'. This program, supported in part by funding from Friends of the Smokies, was designed to expose undergraduate students to the history, politics, ecology, and management of the Park through in-class and

hands-on experiences. From the beginning, we launched the program with the idea that it would be transferable to other institutional frameworks. For this initial offering, students from MTSU took a four-credit, spring semester course, in which weekly class meetings were held on campus. In addition, students spent Spring Break on a front country trip to GRSM, during which they worked directly with Park staff to do a health review of a sedated elk, inventory fish diversity in a local stream, discuss the importance of biological collections to the Park, and interview law enforcement about the challenges of monitoring illegal activity in the Park. The course concluded with a finals week backcountry trip to the Park, in which students learned about backcountry management, the definition of wilderness, and sense of place. Overall, the experience provides students with a perspective of the Park that most people will never have, and it exposes them to potential career paths in a national park setting. We will discuss opportunities for program expansion to other universities in the region.

75 - Take Time to Celebrate: An Impactful Strategy for End-of-Course Reflection

Jennifer T. Thomas

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Ending a course well takes effort. Not only do we hope that our students have learned and can retain the content we have discussed through the semester, we also desire that they can put that material into context with where they are in their studies, how that content contributes to what they know about their discipline, and the impact that their knowledge can have on their community. I have developed an end-of semester celebratory "mocktail" party with a speed-dating format that allows students to reflect on the learning they have accomplished, individually share with others in the class, and collectively share and reflect with the class all that they have learned for the semester. Feedback from multiple courses over several semesters suggests that students desire an opportunity to celebrate their individual and collective experiences and are greatly impacted by the sense of community they share through this reflective process.

76 - Supermarket Botany in the 21st Century

Christopher Hardy

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The use of supermarket fruits and vegetables to teach aspects of plant structure, function or taxonomy is thought to be particularly effective because it can reinforce connections between classroom learning and students' daily exposure to plants. These intuitions, however, have thus far alluded any published critique. Furthermore, the recent emergence and ubiquity of smartphones and biodiversity informatics websites has created new yet unexplored opportunities for student engagement and pedagogy on the subject. For several years, my university botany students have employed their smartphones and one such website, NatureAtlas.org, to extend their study of morphology from the classroom laboratory to the produce isles of their local grocery stores as part of multiple graded "field" assignments. Now, rather than just *hoping* they will apply their classroom knowledge to what they find outside of the classroom, I am requiring them to do so with the taxonomic, photographic and geospatial precision of an ethnobotanist in the field and the technical savvy of a plant morphologist. Students report anonymously that the field assignments enhance their learning and appreciation of plant structure and diversity, and analysis of their observational data bears this out. Equally important, the students' posting of photos and botanical descriptions on NatureAtlas facilitates my assessment of the accuracy of their observations and my discovery of areas of interpretive difficulty that has informed my teaching in ways never before possible. I have further enjoyed the serendipity of learning from my students the market locations and availability of exotic and otherwise hard-to-find fruits and vegetables that might better inform my future selections of produce to bring into the classroom for demonstrations and laboratory study.

77 - Teaching Experimental Design: The value of feedback and constraint in learning higher-order skills

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While it is widely accepted that active learning approaches are more effective at teaching higher order concepts and skills than traditional passive ones, the specific types of active learning that are best suited to maximize learning remains an open question (Freeman et al, 2014). In the course of researching and developing Understanding Experimental Design, an interactive simulation-based lab designed for introductory biology courses, we explored how the degree of open-endedness within an activity influenced student learning. The lab contains a first highly scaffolded ("higher constraint") section introducing the language and concepts behind designing good experiments (variables, controls, replication, etc.) and a second section with lower constraints where students carry out experiments themselves within a simulation environment.

We developed three versions of the second section of Understanding Experimental Design, which varied in the degree of constraint imposed on student actions, and in whether they were provided immediate feedback on their designs. One version had Intermediate levels of Constraint With Feedback (ICWF). A second had the same constraint but No Feedback (ICNF). A third had Lower Constraint with No Feedback (LCNF). We randomly assigned the three lab versions to introductory biology students in two settings - one-on-one with think-aloud interviews, and in a split-class study. We also provided the ICWF version to 27 classes nationwide.

Students showed improvement on lower Bloom's level questions in the first, higher constraint section of the lab, but not on higher Bloom's level questions. In both one-on-one and split-class settings, student proficiency with experimental design post-lab showed the pattern ICWF > ICNF > LCNF, indicating that both feedback and constraint aided student learning. Across the larger nationwide sample, students on average performed similarly, indicating the results are likely to be general. I'll discuss potential implications for the design of active learning exercises.

85 - Endocranial and neuroanatomy of nodosaurid armored dinosaurs (Dinosauria: Ornithischia)

Michael Burns

Jacksonville State University, Jacksonville, AL

Little is known about the endocranial anatomy of armored dinosaurs, due in part to extensive fusion of skull bones in this group. Computed tomography has increased our knowledge of this anatomy, but has not been able to reveal finer details in nodosaurs. Although the chondrocranium has been described for nodosaurids, there have been few descriptions of cranial endocasts. Here, a new specimen allows a description of the detailed anatomy of the nasal cavity, braincase, and otic region in a Late Cretaceous nodosaurid.

Impressions on the roof of the nasal cavity demonstrate anterior and posterior loops of the airway, similar to those described for nodosaurids based on a 3D CT scan reconstruction. Other impressions show that the anterior portion of the airway was highly vascularized, with several prominent parasagittal vessels extending along and perforating the skull roof. The posterior portion of the airway, unlike in the ankylosaurid *Euoplocephalus*, shows no such grooves. This indicates that the mucosa was not intimately appressed to the bone, or that this region was poorly vascularized.

Antorbitally, the airway is flanked by two posterolateral chambers. As has been hypothesized for *Euoplocephalus*, olfaction may have been restricted to these unique chambers. Olfactory turbinates within these chambers are similar to those reported for *Euoplocephalus*. Furthermore, because the medial airways were not involved with this sensory function, the dense anterior vascularization likely served in counter-current heat exchange and/or osmoregulation. This hypothesis is supported by the extensive blood supply to the non-olfactory portion of the nasal vestibule, although an additional acoustic function cannot be dismissed. Extensive vascular irrigation in the looping part of the nasal cavity has been reported for *Euoplocephalus* and another nodosaurid specimen.

Cranial endocasts in *Euoplocephalus* show little variation, so endocranial anatomy may be an important source for phylogenetic characters in derived nodosaurs.

86 - Utilizing do-it-yourself open-source technologies to make easier the life of the field herpetologist

Patrick Cain

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Field herpetologists are commonly required to fix, slice, hack, and modify field equipment to meet the needs of their research question. Not only does much of a field herpetologist's training lack formal introduction to such methods, the cost of commercially available technology may also preclude certain unique or informal approaches to answering biological questions. Here, I present a primer on ways one can learn to become more familiar with and skilled at modifying common electronic field equipment. More specifically, I will introduce how open-source hardware and software (e.g. Arduino, Raspberry Pi, and Python) and the thriving do-it-yourself (DIY) community can help facilitate such skills. With just a cursory understanding of electrical engineering, soldering, circuits, and coding, field herpetologists can overcome many of the limitations of cost, and even develop customized field equipment themselves. I will briefly discuss few examples of open-source do-it-yourself equipment such as environmental loggers, GPS data loggers, and VHF systems (transmitters, receivers, and antennas).

87 - Harnessing Citizen Science to Address Data Deficiency in Understudied Herpetofauna: Lessons from the Mountain Chorus Frog (Pseudacris brachyphona)

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Data deficiency in herpetofaunal conservation is often driven by an abundance of private lands that are inaccessible to traditional surveys, precluding adequate assessments of the conservation status of individual taxa. Citizen science approaches are one avenue that may allow researchers to circumvent landownership issues, although little information exists to date to test such approaches' efficacy, especially when applied to secretive taxa. We used a citizen science initiative to address data deficiency in the Mountain Chorus Frog (*Pseudacris brachyphona*) across an area composed primarily of privately-owned lands in the southern Cumberland Mountains ecoregion. We trained more than 500 citizen observers in performing auditory surveys for this species during 2018 and 2019. Those observers increased the number of known localities of Mountain Chorus Frogs in our study area from 14 to nearly 50 within a single breeding season. We found that breeding habitats for Mountain Chorus Frogs across our study region are primarily pools that are not included in state and federal wetlands inventories, being significantly smaller and more isolated than sites identified in remotely-sensed datasets. These results indicate that data deficiency in this species may be driven in part by breeding habitats that are difficult to remotely identify, many of which occur on private lands and do not meet regulatory thresholds designed to protect wetland habitats. More broadly, our results underscore that citizen science approaches can both enhance the natural history knowledge of understudied amphibian taxa and highlight gaps in conservation policy.

88 - Is the Decline in Bats that Use Southeastern Caves Causing Salamanders to Decline as Well?

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White-nose Syndrome, first documented in the US in 2006, has been implicated in recent, precipitous declines in the populations of bats that frequent caves as hibernating refugia. In Georgia caves, bat counts in winter hibernacula dropped by more than a third within one

year of the disease's discovery in the state (2013). Within four years, hibernacula counts had dropped by 95%. Using visual-encounter surveys, we counted salamanders within some of these same caves for 19 consecutive years, a time period which overlaps the decline in bats. Although not as drastic, our data indicate a significant decline in salamander numbers within these caves across both species and seasons. While our analysis is not conclusive, it is strongly suggestive of a connectivity between bats and salamanders. Many cave invertebrates, which serve as salamander prey, rely on the input of energy provided by guano within cave systems. Moreover, guano is a significant source of nutrients for at least some aquatic, troglobitic salamanders, which ingest guano directly. We recommend (1) investigations into food webs linking the possible importance of bat guano to salamanders; and (2) robust monitoring programs for cave-using salamanders, especially species of conservation concern.

89 - Effects of Road Mortality and Traffic Noise on Pool Breeding Amphibians

Nicholas Shieler

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Roadway mortality is of increasing interest to conservationists, and anthropogenic disturbances are a leading cause of species loss. Species with high vagility, like pool breeding amphibians, may be especially susceptible to mortality on roads since they often cut across annual breeding migration paths. The potential effects of anthropogenic noise are also of increasing interest to conservationists, and roadside noise from traffic may affect the calling behavior of anurans that breed in in nearby pools and ditches. With this study, I examined the effects of roads on pool breeding amphibians through a two-pronged approach. I monitored roadkill via visual road surveys and reproductive success via larval trapping in vernal pools in salamanders of the genus *Ambystoma* at low traffic, high traffic, and reference sites. I also used an experimental protocol to examine the effects of traffic noise on the calling behavior of two anurans of the genus *Pseudacris*, spring peepers (*Pseudacris crucifer*), and mountain chorus frogs (*Pseudacris brachyphona*). Anuran recordings were analyzed to identify changes in call intensity, frequency, duration, and pitch in the presence of traffic noise. The record of road-kills over the last two seasons suggests that large numbers of pool breeding amphibians succumb to traffic each season. The results of this study could influence conservation and management decisions, and lead to increased efforts to mitigate loss and decrease anthropogenic soundscape disruption.

90 - Use, Abuse, and Misuse of the Term "Diffusion" in the Classification of Membrane Transport Mechanisms

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The most difficult task in teaching Natural Sciences at Higher Education level is to decide what not to teach. The other difficulty is to teach what the students need according to their majors, based exclusively on their previous knowledge. This becomes particularly important when teaching courses in Biology and Human Anatomy and Physiology to freshmen and sophomores while they are still taking their Basic Sciences courses (Mathematics, Chemistry, and Physics). In the case of the topic of Membrane Transport Mechanisms, the term "Diffusion" is correctly used when it refers to the net flux of a substance (ion or molecule) from a region of higher concentration to one of lower concentration. However, it is rarely or not at all stated that no mechanical barrier, like the cell plasma membrane, may be present. The term is further abused and misused when the flux of a lipid-soluble molecule occurring down its concentration gradient through the lipid bilayer of the plasma membrane is named "Simple Diffusion". This is also the case when the flux of a hydrophilic substance taking place down its gradient (concentration for molecules; electrochemical for ions) through an integral membrane protein (a transporter) is called "Facilitated Diffusion". These two membrane transport mechanisms have to be correctly named as "Simple Permeability" and "Passive Transport by Transporters", respectively. "Diffusion" is a very well described physical phenomenon, both qualitatively and quantitatively (for example, Fick's First and Second Laws), with no mechanical barrier present and no saturation of the flux while increasing the gradient.

91 - Y353A Mutant Uncovers Potential Transmembrane Contribution to SpNox Substrate Binding

Nicholas Wilson

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Human NADPH oxidases (hNOXes) are a family of eukaryotic enzymes that produce reactive oxygen species (ROS). These transmembrane enzymes move electrons from NADPH to FAD in the dehydrogenase (DH) domain, and then across the membrane via their transmembrane (TM) domain to the final electron acceptor O2, forming the superoxide anion O2-. The misregulation of Noxes is associated with diseases ranging from diabetes to cancer. SpNox (*Streptococcus pneumoniae* NADPH oxidase) is a recently discovered prokaryotic NOX homolog that can serve as a model system for the study of the NOX family. While hNox has a preference for NADPH over NADH, this same selectivity is not seen in spNOX. Evidence from DH homologs suggests that a tyrosine (Y) at the 353 position SpNox interacts solely with the adenine ring, conferring a preference for NADH as the substrate. Meanwhile, an arginine (R) in this position confers preference to NADPH which would allow it to interact with the 2' phosphate. This study investigates the binding affinity of both full length and dehydrogenase domain for NADH and NADPH when Y353 is mutated to R or alanine (A).

Results from the study indicate a decreased Michaelis constant (Km) of NADPH in both the wild-type (WT) and DH constructs when mutated with R which suggests the importance of pi stacking in this enzyme. An increased Km from the NADPH in the A mutant serves to highlight the importance of pi stacking in substrate binding for this enzyme. Most interestingly, a 10-fold decrease in the catalytic efficiency of the Y353A mutant compared to the WT DH construct uncovers the potential contribution of TM domain in substrate binding. Future studies are dedicated to understanding the complete mechanism of substrate binding to spNOX and the contribution from its domains.

92 - Structure-function Studies of Fibronectin Binding Proteins from Relapsing Fever Spirochetes

Charles Booth

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The *Borrelia* genus is comprised of many spirochetes, with some species causing disease in humans. One such pathogen is *Borrelia burgdorferi*, the causative agent of Lyme disease. *B. burgdorferi* expresses an outer surface lipoprotein, BBK32, in which the N-terminus binds mammalian fibronectin contributing to adherence of *B. burgdorferi* during infection and promotes spirochetal extravasation. Meanwhile, the C-terminus contributes to evasion of the host's innate immune system by inhibiting C1r, the initiating protease of the classical complement pathway (CP). Another disease caused by related spirochetes of the *Borrelia* genus is Relapsing Fever (RF), and phylogenic analysis shows that there are up to three separate BBK32 orthologues encoded by RF spirochetes which are termed FbpA, FbpB, and FbpC. Given their relatively conserved overall sequence identity to Lyme BBK32, we hypothesized that these RF spirochetal proteins may also contribute to CP evasion. To test this hypothesis, biochemical assays, structural biology, and surface plasmon resonance (SPR) were used to evaluate inhibitory and binding interactions of RF Fbp proteins. Our findings suggest that FbpA inhibits like BBK32 with an IC_{50} approximately 23 nM in serum-based assays. FbpB does inhibit in non-serum-based assays with an IC_{50} 12nM, but does not inhibit within serum-based assays. Lastly, FbpC does neither bind nor show any inhibitory function with regards to CP. This data suggests that the underlying differences in protein sequence and structure of RF Fbp proteins may contribute to a molecular mechanism for host-tropism, and contributes to a difference in the inhibition of the C1r protease.

93 - Re-Endothelialization of Porcine Internal Thoracic Artery Scaffolds for Vascular Tissue Engineering

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Cardiovascular disease (CVD) exerts a consistent burden of morbidity and mortality. For CVD patients that require remediate cardiovascular materials, synthetic and crude biologic valvular and vascular materials are traditionally employed. However, these solutions are fundamentally limited. Issues of physiological integration restrict the use of synthetic grafts whereas biological graft solutions, such as allografts and xenografts, are not reliable for many applications due to the immune response they frequently illicit. Continued development of alternative graft solutions is, therefore, of tremendous relevance. These new fabrications should ideally be expedient to manufacture, have low immunogenicity, adequately perfuse tissues, and be exceedingly durable. Tissue engineering – the utilization of life science and engineering principles in tandem towards the understanding of biological structures – is an approach well suited to the development of such vascular solutions. Decellularized porcine tissues hold great promise as scaffolds for human tissue engineering. The decellularization process reduces the graft's immunogenicity while maintaining key structural elements, and repopulation of the scaffold with the appropriate human cells can restore anatomical and physiological function. Yet, within this process, many questions of optimization remain unanswered. We hypothesized that increasing the concentration of decellularization agents negatively affects the ultrastructure of the resulting scaffold and the efficacy of its recellularization. To test this hypothesis, segments of porcine internal thoracic artery were decellularized in 0.5-3% sodium deoxycholate/sodium dodecyl sulfate solutions. The ultrastructure of the decellularized tissue was evaluated via scanning electron microscopy. Scaffolds were recellularized with endothelial cells according to a standardized protocol, and the efficacy of the recellularization was evaluated via metabolic and histological analysis. Our results indicate that increasing detergent concentration increases scaffold porosity while decreasing scaffold biocompatibility. These results highlight the importance of carefully titrating decellularization conditions for tissue engineering applications that rely on acellular tissue-derived scaffolds.

94 - The effects of CRISPR-cas9 mediated gene knockout of WntA gene in Vanessa cardui wing patterns and pigmentation

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Genes that regulate wing patterning and color in different butterfly species is a tractable mechanism to understand both developmental genetics and speciation. With the use of CRISPR-based gene editing, we can now probe gene function through targeted knock outs of genes known to contribute to wing morphology. The focus of this project is the wing patterning gene, *WntA,* in *Vanessa cardui.* Deactivation of the *WntA* gene using the CRISPR-cas9 technology results in increased melanisation and a loss of patterning in both the dorsal and ventral sides of *V. cardui* wings. We deactivated the *WntA* gene through the CRISPR-cas9 mechanism using two, previously untested, target sequences. In order to deactivate the *WntA gene,* guide RNAs were designed to new areas of the *WntA* gene using wild-type *V. cardui* gene sequence, then injected into *V. cardui* eggs with Cas9 endonuclease. Phenotypic analyses of injected butterflies using the novel guide RNAs noted melanisation of pigment and patterning changes. Genotypic analyses of phenotypically mutated butterflies revealed deletions of varying degrees at or around the new target sequences.

95 - Effects of pine litter raking and burning on plant community composition and soil seed banks in longleaf pine savannas

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Longleaf pine savannas are a fire-dependent ecosystem with high understory diversity. Landowners manage longleaf pine savannas for the raking and subsequent sale of pine litter. Although raking is a widespread practice, its effect on longleaf pine ecosystems is understudied. We investigated the effects of raking and burning in longleaf pine savannas on understory plant community composition and soil seed banks at the McCain Forest Management Area in Hoke County, North Carolina. In each of five sites, with different combinations of raking and burning histories, we established 10 80 cm x 120 cm plots. Each plot was divided into six quadrats; three were sampled in May 2019 and three were sampled in September 2019. We measured litter depth, estimated percent cover of understory species, and collected four 3 cm deep soil cores, which were homogenized to create one aggregate soil sample for each quadrat. For the September sampling event

we had three soil treatments: a control, a cold treatment of 8 °C, and litter collected with soil. To assess the seed bank, soils were spread in pots, watered daily, and monitored for germination. We found that there was no effect of raking or burning on litter depth. Percent cover of the two most common understory species, wiregrass (*Aristida stricta*) and dwarf huckleberry (*Gaylussacia dumosa*), did not differ between raked and unraked areas or between burned or unburned areas. There were only 10 and 12 germinants in the May and September seed bank studies, respectively. Low seed germination, regardless of raking and burning history, suggests that longleaf pine savannas do not have long-lived soil seed banks. Overall, our results indicate that raking does not seem to affect the composition of the understory plant community or the soil seed bank in longleaf pine savannas.

96 - Are fire temperatures and residence times good predictors of survival and re-growth for resprouters in Florida scrub?

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Resprouting is a widespread adaptation allowing plants to persist in disturbed ecosystems. Resprouting is common after fires, but resprouting percentages and vigor vary with fire intensities and environmental conditions. Resprouting is prevalent in Florida scrub and associated plant communities, but no studies in these systems have thoroughly quantified resprouting in relation to fire. We established 16 transects in areas slated for burning at Archbold Biological Station, marked random plants, recorded plant sizes before fires and after (6 months, then annually for up to eight years), and used dataloggers to quantify burn temperatures and residence times at ground level. We accomplished 15 fires across five years, encompassing 60 common resprouting species. Maximum temperatures ranged from 47-890 degrees C (mean 549), with residence times ranging from 0-83 minutes (mean 10). Resprouting was strong (89%) and first year survival also was high (88%). After the first year, cumulative survival was 97%. Although survival was affected by fire temperatures and residence times, the effects were non-linear, with no tendency for decreased survival in more intense fires. Survival varied nonsignificantly by species group, with palmettos having nearly 100% survival. Post-fire growth was very high in the first year and slower thereafter. Relative growth rate at six months was unaffected by fire but varied among species groups. Most species recovered pre-fire size by five years, with palmettos recovering the fastest. This study shows Florida scrub plants are resilient to a range of fire intensities; a previous study showed resilience to a range of fire frequencies. However, some species (e.g. palmettos) will be able to take advantage of more intense or frequent fires and this could eventually shift species composition. Because obligate seeding species are much more sensitive to the fire regime than resprouting species, land managers will need prioritize their needs in developing prescribed fire regimes.

97 - Long-term landscape-scale homogenization and decoupling of community-environment relationships following logging in the southern Appalachians

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Widespread logging occurred throughout the eastern United States by the early 20th century. Despite the extensive nature of logging, studies addressing questions about the long-term impact of logging have been limited by scarcity of historical land-use data and rarity of forests without a history of intensive human disturbance. But how has this widespread disturbance changed how forests are structured on the landscape? It is well known that climatic and topographic factors have a strong influence on community composition and structure in forests in this region, but the logging signature on these relationships is unclear.

We explored this question using the documented land-use history of Great Smoky Mountains National Park (GSMNP), which maintains some of the largest tracts of old growth forest in the eastern US. We used Generalized Dissimilarity Modelling (GDM) and data from several vegetation studies to address questions about the relationship between beta diversity and logging history. Measuring beta diversity is particularly important considering biotic homogenization, the increased similarity of regional biota, can occur for decades following human disturbance. Beta diversity also provides important insights into the processes that shape communities and patterns of biodiversity, which is particularly important in the southern Appalachians given the highly variable communities in the region.

We found that logging changes the long-term relationships between space/the environment and vascular plant species turnover (one aspect of beta diversity). Specifically, logging increased the importance of spatial factors, and decreased the importance of environmental/topographic factors in structuring communities. Additionally, logging resulted in long-term homogenization of forest communities on a landscape scale. Our results provide information on the specific drivers of differences between old growth and logged forests which is invaluable for informing forest management, conservation and, remediation.

98 - Thermal Range Specialization in Tropical Bees

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There is an urgent need to document thermal range tolerances and specialization in tropical bee assemblages to understand how important pollinators may respond to warming temperatures, as tropical ectotherms are expected to be the most vulnerable group. Our long-term study (2012-2019) aims to quantify patterns of thermal range specialization and peak abundance in tropical bee communities. We focus on 17 bee species from the stingless bee tribe, Tribe Meliponini, as this is an economically important bee tribe throughout the tropics owing to their production of wax and honey. Although their specific contribution to pollination has not been quantified, they are likely one of the most important pollinator groups in tropical forests because they are social and have higher abundances locally compared to their solitary counterparts.

Three adjacent roadsides were used as elevational transects in the seasonally dry Pacific slope forests of Costa Rica. The study area represents a mixture of smallholder farms, pasture and forest patches, and is located in a conservation area. Bees were sampled at each

100m elevation change using hand collection methods and a honey spray solution.

A distance-based redundancy analysis indicates that elevation and site explain 52% of the variation in Meliponini community composition ($F_{pseudo}(1,8) = 3.75$; $P = 0.005$). Mountain-dwelling species are expected to exhibit shifts to higher elevations and cooler temperatures over time due to global temperature increases.

Our study is one of the first to provide evidence of thermal range specialization in several bee species. These findings indicate that bee species of tropical montane landscapes could be at high-risk to warming temperatures or changing patterns of precipitation, as elevation is a strong factor in shaping stingless bee communities. More work is needed to understand how these changes in the bee community may affect crop production and which species are the most vulnerable.

99 - Impacts of Invasive Ailanthus altissima on Woody Plant Communities in an Old Growth Forest of Southeastern Kentucky

Hailey Mount[1], Jennifer Koslow[2]

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The non-native tree *Ailanthus altissima* (Simaroubaceae), or Tree-of-Heaven, is a competitive and widespread invasive species in the United States. The growth and spread of this species is primarily limited by the amount of light available. Because of this light requirement, canopy gaps are crucial points for the introduction and spread of *Ailanthus* into forests. Other studies have recorded decreases in native species diversity of the herbaceous layer after invasion of relatively disturbed landscapes, although there was greater overall diversity in invaded plots. The current study examines these impacts as they appear in woody species composition in an old growth forest setting in Appalachia. At the study site, Lilley Cornett Woods in Letcher County, Kentucky, nine invaded gaps were compared to nine nearby univaded gaps. Belt-transects were run through paired canopy gaps, the presence of woody species was recorded, and some properties of the area like soil pH and gap size were measured. The characteristics of species that were most common at either invaded or uninvaded gaps, such as tolerance to soil pH, gap-response, and successional status were assessed. As with previous studies, there was higher soil pH at the sites where *Ailanthus* was present. More significantly correlated with *Ailanthus* presence was overall Shannon diversity, and native species diversity per site which, unexpectedly, increased at invaded sites. Compared with the previous studies, impacts in native species composition appeared less severe amongst the woody species, and introduction was confined to canopy gaps in forested settings. These data also support the resilience of old growth forests to invasion by non-natives. Because native diversity was able to increase, and persisting species were classified as generalists, it may be the case that due to its great heterogeneity of native species and species competition, invasion by *Ailanthus* can be combated by previously suppressed native plants.

100 - A CURE for your Curriculum

Judy Awong-Taylor, Clay Runck, Allison D'Costa

Georgia Gwinnett College, Lawrenceville, GA

CURE-rious? Come Check us out!

101 - Undergraduate Investigations of Antlion Feeding and Behavior

Patrick Cain, Mark Schlueter

Georgia Gwinnett College, Lawrenceville, GA

We created a CURE project that utilizes antlions, which are also sometimes referred to as doodle bugs. Antlions are insects in the Family Myrmeleontidae and are best known for the fierce prey-capturing behavior exhibited by their larvae. The main goal of the following proposal is to create a CURE project that utilizes antlions in the introductory BIOL 1108K course to help increase student engagement. In this project, we introduced BIOL 1108 students to the biology and behavior of antlions. The specific focus of the project initially was the predatory behaviors and feeding habits of the antlion larvae. Students in each class were divided into groups of three or four to complete the initial project, after which the students developed a second experiment of their own design. We compared survey data covering basic biology, experimental design, and antlion biology between three BIOL 1108 sections that used antlions and two sections that conducted corn growth experiments (control groups). BIOL 1108K has three STEM skills assigned to it (data analysis, effective communication, ability to apply evolutionary concepts). Thus, during this research project, students gathered raw data in their experiments and then used t-tests and ANOVA to compare, contrast, and interpret data. Students also practiced their "effective communication" by writing a scientific paper. Evolutionary concepts will be explored, discussing the ecology and evolutionary principles behind the predatory tactics of the antlion larvae. While antlions are generally easy to work with, observing predatory behavior is always challenging.

102 - Scaffolding CUREs in an Introductory Biology Lab

Barbara Musolf, Ann Showalter

Clayton State University, Morrow, GA

Convincing students that they can be scientists and contribute to science can motivate them to persist and succeed in the sciences. Course embedded undergraduate research experiences (CUREs) in students' first year of taking biology courses gives them an opportunity to design and carry out authentic research. Students are introduced to the process as they carry out an experiment that is designed by the entire class. They then repeat the process when they design another experiment in small groups of 3 or 4 students. We use the naming of variables as the foundation to scaffold the knowledge and skills needed to carry out a study. We practice producing good variable

names and show them how well-defined independent and dependent variables can be used to craft a clear hypothesis and prediction. In developing methods, they are introduced to the importance of controlling variables that may lead to confounding their results. Once they have designed their methods and determined an appropriate sample size, they are ready to carry out their experiment and collect data. The analysis of the data also relies on knowledge of their independent variable. They are taught appropriate graphs to use based on whether their independent and dependent variable is categorical or quantitative. The same variable distinctions operate when they decide what statistics they will use to analyze their data. In the final part of their research experience they use scientific literature to determine how their study contributes to our understanding of their model organism. They then communicate their findings individually in a scientific paper that is in a journal format and as a group, they design and present a poster on their findings.

103 - Effect of CURE projects on written communication skills in gateway biology course

Takayuki Nitta, Andrew Methven, Xiaorong Zhang, Andrea L. Moore

Savannah State University, Savannah, GA

Savannah State University (SSU) is a public historically black university in Georgia. The department of Biology at SSU introduced two CURE projects, (1) Quantitative Analysis of Organic Molecules in Foods and (2) Algal Growth Experimentation to transform traditional organic molecules and plant labs into mini-research projects in the BIOL 1107L – Principles of Biology I Lab. These CURE projects were designed to reinforce theory related to organic molecules and photosynthesis, engage students in experimentation and data analysis, and provide inquiry-based activities to bridge several core ideas in BIOL 1107, which would aid in student success and retention rates. The first CURE project, organic molecules lab, requested our students to hypothesize types and amount of organic molecules they selected, implemented the research protocol and analyzed experimental data to determine the protein and carbohydrate content of each food. The second CURE project was adapted from the Algae to Energy: Optimizing Systems lab by Boyce Thompson Institute. In the project, students designed and conducted an experiment that manipulated one or more variables involved in growing algae (CO_2, light and/or nutrients) and measured algal growth with a spectrophotometer and/or hemocytometer. The SSU CURE team assessed students' ability to apply the process of science, specifically, to design experiments using the Experimental Design Ability Test (EDAT) and their description of the experiment in lab reports across control (traditional labs) and experimental (CURE) groups. We here assessed the two reports which were written by the students through the course. The reports are expected to describe some fundamental factors in science written communication (e.g. statement of questions, hypothesis, methods, data presentation, interpretation). The data analyzing the reports with our rubric and how our CURE projects influence students' skills in written communication will be presented in the conference.

104 - Connecting Metabolism to Catalase Function: A CURE for Introductory Biology

Ann Showalter, Indhira De La Rosa, Barbara Musolf, Paul Melvin, Michelle Furlong

Clayton State University, Morrow, GA

To address student success challenges and implement the recommendations of Vision and Change, we have been transforming the curriculum of our major's introductory laboratory laboratory course by including course-embedded undergraduate research experiences (CURE) and other high-impact teaching practices. During the first phase of our CURE transformation, we developed the framework for effectively teaching basic experimental design and data analysis skills using yeast catalase as our focal system. We are currently moving into the second phase of the CURE transformation by bringing back many of the technical skills and knowledge required for molecular/cellular research. We have expanded our focus on catalase function in yeast by connecting this topic with yeast metabolism. Although we have only implemented these changes in the last semester, our students are developing more sophisticated experiments that require greater knowledge and skill in molecular/cellular biology.

105 - Assessment of microbial diversity in a "Pond in a Jar" ecosystem

Chris Gissendanner, Timothy McMahan, Srinivas Garlapati, Tom Sasek

University of Louisiana Monroe, Monroe, LA

Microbial diversity is an important component of all ecosystems. In humans, disruption of the microbial ecosystem of the gut can lead to serious health consequences. We have designed a CURE that investigates the effects of environmental disruption on the microbial diversity of a laboratory "pond" ecosystem. This CURE is an update of a "Pond in a Jar" project that has been a part of the introductory biology lab course at ULM for over 15 years. In the updated CURE, students utilize microbiological techniques to quantitatively and qualitatively assess microbial diversity following chemical disruption of the ecosystem. We intend for this CURE to address the following STEM skills: 1) Ability to apply the process of science; 2) Scientific communication; and 3) Data analysis. Experience from the initial implementation of the CURE led to revisions to better guide students in quantitative analysis and interpretation of results. The current version also incorporates identification of bacteria by 16S rDNA sequencing. We will present the results of this ongoing effort.

106 - Quantitative Analysis of Organic Molecules and Optimizing Algal Growth

Andrea L. Moore, Xiaorong Zhang, Takayuki Nitta, Andrew Methven

Savannah State University, Savannah, GA

As a part of the Vision and Change movement, a team of biology faculty at Savannah State University have begun to redesign the introductory biology labs to include a component where students apply the process of science through CUREs. The team has developed and implemented two CUREs that transform the traditional cookbook labs into two short mini-research projects designed to answer real world questions. The first, Quantitative Analysis of Organic Molecules in Foods and the second, Photosynthesis: Algal Growth Experimentation are aligned to the student learning outcomes for the lecture class and provide skills that will be used in successive courses. Quantitative

Analysis of Organic Molecules measures the protein and carbohydrate concentrations in food using the spectrophotometer. Photosynthesis: Algal Growth Experimentation, a modification of Algae to Energy: Optimizing Systems lab by Boyce Thompson Institute, allows students to manipulate variables to optimize the growth of *Chlorella*. The CUREs allow students to apply the scientific process, analyze data, and write for the sciences. Both CUREs can be scaled up to full semester projects.

107 - Implementation of a semester-long, cell culture and fluorescence microscopy CURE with an underrepresented STEM student population

Jennifer Hurst-Kennedy, Michael Saum, Cindy Achat-Mendes, Allison D'Costa, Elisabeth Javazon, Shoshana Katzman, Ernest Ricks, Jr., Alessandra Barrera

Georgia Gwinnett College, Lawrenceville, GA

Georgia Gwinnett College (GGC) is an access institution with a diverse student body, located in metro Atlanta. To strengthen research skills, teach employer-valued cell biology laboratory techniques, and increase student engagement; a semester-long, inquiry-based CURE was developed and implemented in Cell Biology with Laboratory (BIOL3400K), a sophomore-level course, which serves as a "gateway" to all upper-level Biology courses. This CURE centers on the investigation of a student-chosen experimental factor on the viability of cultured, mammalian cells. Through participation in this CURE, students gain experience in cell culture, fluorescence microscopy, and viability assays, and strengthen important research skills, such as literature searches, graphing, and data analyses. The impact of this CURE on student learning gains and attitudes was assessed using a pre-/post- content exams and the Colorado Learning Attitudes about Science Survey (CLASS). Our data show that all students made significant content gains. Female students made larger learning gains than male students. Additionally, minority students performed better than majority students in some content areas. Student attitudes did not change, or in some cases were slightly more negative after the CURE. Overall, this CURE had a positive impact on students by engaging them in an inquiry-based laboratory experience.

108 - Biotechnology Applications in the Detection of Genetically Modified Foods

Ernest Ricks, Jr., Cindy Achat-Mendes, Jennifer Hurst-Kennedy, Robert Haining

Georgia Gwinnett College, Lawrenceville, GA

This CURE provides students the opportunity to learn and use leading techniques in biotechnology, while strengthening their understanding of the central dogma of biology, and facilitating an authentic research experience. In one module, students can use PCR to detect the presence of common genes found in genetically modified (GM) foods. In a second module, students can isolate messenger RNA, synthesize cDNA, and employ real-time quantitative PCR to investigate the expression of GMO genes. The last module utilizes Enzyme-Linked Immunosorbent Assay (ELISA) to detect the presence of GM proteins. Students receive training in lab research/STEM skills including troubleshooting equipment, experimental design, maintaining a lab notebook, writing manuscript-style lab reports, and oral presentation of research findings. Students are required to know the purpose of reagents and procedures rather than follow cookie-cutter recipes. They learn the theory and application of PCR, real-time PCR, and ELISA to investigate the relationship between genes, RNA and proteins, respectively, in GM foods. This CURE resulted in over 20 campus and regional conference student presentations over the past 3 years. The effectiveness of this project was assessed by evaluating gains in *student learning and student attitudes* towards research and STEM careers. Assessment tools included: *a) pre- and post- content surveys* (multiple choice questions that are linked to course learning objectives), *b) 4-year URE student survey*, and *c) Lab report rubric designed by the Biology Faculty.* The attitudinal survey data suggest that following participation in the GM foods lab design students: 1) Became more knowledgeable about the testing of genetically modified foods and central dogma; 2) Appreciated designing and taking ownership of their own research project; 3) Expressed better understanding of research in the biotechnology field. Significant outcomes of this new lab curriculum include student-initiated hypothesis-driven authentic research projects, troubleshooting and critical thinking as students worked through technical challenges.

109 - Assessment of CUREs

Tirza Leader

Georgia Gwinnett College, Lawrenceville, GA

Assessment is a crucial piece of any experimental design, classroom experience, or innovation. However, creating an assessment that successfully and effectively evaluates complex programs that utilize multiple and innovative research designs, as well as the individual classroom experience requires an interdisciplinary skill set and tools. The presentation will walk through the assessment process created for 4-year Undergraduate Research Experience program at Georgia Gwinnett College. Strengths and weaknesses of different forms of assessment will be discussed, and examples of successful and less than successful assessments will be provided.

111 - Using machine learning algorithms to aid in detection and identification of cryptic species.

David S. McLeod[1], Li Xu[2], Eric Smith[2], Yili Hong[2]

[1]James Madison University, Harrisonburg, VA, [2]Virginia Tech, Blacksburg, VA

As biologists we seek to recognize and understand the biodiversity of the natural world. At times, species identification is confounded by morphological similarity especially among organisms comprising species complexes. The ability to use a device to detect and accurately identify unknown organisms in our environment was, until recently, relegated to dreams and science fiction writing. Image recognition, machine learning, and the algorithms that power them are becoming increasingly more sophisticated and accessible. In recent years these technologies have progressed to the point that with a cell phone and an app any individual can capture an image of an organism

have it positively identified both by a computer and a community. We present preliminary results from the development and application of a machine learning method used to aid in species identification and delimitation. We demonstrate the potential to use natural, species-specific, patterns in morphology to simply and accurately identify members of a species complex. Additionally, we consider the utility of the neural network in transforming qualitative morphological traits into quantitative ones that can facilitate the establishment of discrete species boundaries and aid in species identification.

112 - Anuran breeding in a small-town urban environment in Northeastern Alabama

George Cline, Brenda Cline

Jacksonville State University, Jacksonville, AL

Alabama is geographically and physiographically diverse. The physical variety lends itself to increasing biodiversity. Alabama has the highest biodiversity for states east of the Mississippi River (Duncan 2013). Herpetologically speaking, the state is influenced by the Appalachian Mountains in the NE and the coastal plain to the south. Jacksonville is nestled along the western slopes of the Appalachian Mountains in the Ridge and Valley Province. The Anuran community reflects both these influences as they meet in Jacksonville. The city was divided into 4 quadrats: NE, SE, SW, NW. City streets were driven been dusk and midnight 3-5 times perweek over a 2- year period. Ten species representing 4 Families of anurans were observed across the city over that period. Hylid frogs and Ranids dominate the communities. One species, *Hyla chrysoscelis*, was spread nearly evenly across the city. *Anaxyrus americanus* was also broadly spread, but it had a patchier dispersion. Ranids were restricted to a few permanent ponds in the southeastern quadrat. Only one specimen of *Scaphiopus* was found. This species is secretive and patchy at best. Only one other site for *Scaphiopus* has been recorded in town: both sites were in the NE quadrat. Breeding phenology was compared across years. Patterns varied annually and correlated with rainfall patterns.

113 - Preliminary Analysis of Invasive Flora Impacts on Home Range Size in a Long-Lived Ectotherm Vertebrate

Kayla Bonadie, Amber Rittgers, Natalie Hyslop, Jennifer Mook, Abigail Neyer

University of North Georgia, Oakwood, GA

Habitat loss, fragmentation, and degradation can restrict animal movements by creating barriers of unusable matrix in home ranges. Invasive plant species contribute to this disturbed matrix by disrupting landscape structure through replacement of native vegetation and may impact animal movement, potentially impacting gene flow and population fitness. Changes in habitat composition and resource availability from the presence of invasive plants may have implications for imperiled vertebrate species, particularly long-lived ectotherms given their reliance on availability of specific thermal conditions influenced by habitat conditions. Thus, research on these species may provide insight into conservation and management practices for invasive-impacted ecosystems. To investigate environmental factors that influence movement patterns and habitat use, including influence of a widespread invasive plant species, we have conducted a radio-telemetry study on Eastern Box Turtles (*Terrapene carolina*) since 2013. The study site, a 31-hectare plot in the Northeastern Piedmont region of Georgia, is composed of mixed hardwood-pine uplands, mesic and upland areas dominated by Chinese privet (*Ligustrum sinense*), beaver-created wetlands, and human maintained areas. To date, we have radio-tracked 36 turtles which we locate by homing 1-6 times per month, with an average of 60 radiolocations (range: 1 to 199) per turtle. Upon location, each turtle's microhabitat use is assessed in a 1.5-meter diameter plot by quantifying understory vegetation and other local habitat components. Minimum convex polygons were used to estimate annual home ranges, which we relate to microhabitat use. Annual home range size varied from 0.86 ha to 10.3 ha and averaged 3.8 ha. Our preliminary analyses show that across multiple years there was a negative trend present between proportion of microhabitat composed of privet and home range size. Our data on habitat use, home range and microhabitat structure may help to identify factors that are impacting species persistence and resource use in vulnerable ectothermic populations.

115 - Impacts of Climatic Variables on Annual Cicada Emergence in Relation to Seasonal Abundance of Eastern Copperheads (Agkistrodon contortrix)

Jesse Sockman[1], Josh Hendricks[2], Renae Steinberger[1], Stephen C. Richter[1]

[1]Eastern Kentucky University, Richmond, KY, [2]Florida Fish and Wildlife Conservation Commission, Perry, FL

For many species, life history events are cyclical and often correspond to specific environmental conditions. As a result of environmental variability, the optimal conditions that regulate the range and activity of highly regulated cyclical organisms, like cicadas, are subject to temporal change. Variability in cicada emergence and abundance has been shown to impact the species that rely on the rapid influx of nutrients. One such predator is the Eastern Copperhead (*Agkistrodon contortrix*) that has been noted feeding on emerging cicadas throughout their range. In eastern Kentucky, observations of copperheads congregating to feed on cicadas has been documented in recreational areas. This creates an urgency to understand the driving factors of the timing of this relationship to reduce negative human-copperhead interactions. The objective of our research was to investigate climatic variables (temperature, humidity, precipitation, and growing-degree days) in connection with the timing of copperhead movement and cicada emergence. Nightly visual encounter surveys were conducted to determine copperhead and cicada relative abundances while observing behavioral interactions. Climatic data and environmental factors were collected during each survey or through the Midwestern Regional Climate Center and US Naval Observatory. Each year copperheads congregate consistently after the initial rush of cicada emergence with arrival fluctuating only a day across three years. Preliminary results indicate that copperhead abundance is positively related to temperature, growing degree day accumulation, and emergence of cicadas. In contrast, cicada abundance was inversely related to temperature and growing degree days. This may be due to the pulsating nature or a thermal optimum of cicada emergence, which will be the focus of further analyses. Overall, analyses suggest that cicada emergence within the site is a preemptive indicator of copperhead abundance.

116 - An investigation of the genetically modified tortilla chips served at fast food restaurant chains

Gabriella Tyler, Katherine Brubaker, Amanda Harless, Kristen Donahue, Kenneth Levenson, John Senat, Stephany Sifuentes, Ernest Ricks, Jr.

Georgia Gwinnett College, Lawrenceville, GA

Public awareness of genetically modified organisms (GMO) present in consumables has led to the reformation of food labeling standards as outlined by the United States Department of Agriculture (USDA). As of January 01, 2020 the USDA put a new labeling measure called the National Bioengineered Food Disclosure Standard into effect. It mandates that any ingredient within a product containing >5.0% of a bioengineered substance must be labeled for consumer awareness. A GMO is an organism who's DNA has been bioengineered to become resistant to herbicides, pesticides, and insects. (Elenis, et al. 2008) If a crop has been modified to resist these compounds they will continue to grow and produce even when they are saturated. GMO's raise cause for concern, as the long-term implications of consuming foods, which have been exposed to large volumes of chemicals, are unknown. We attempt to elucidate whether fast food conglomerates are serving corn tortillas chips composed of GMOs to unaware customers. Four restaurants were investigated in this study: Moe's, Taco Bell, Chili's, and Chipotle. We screened for the following common corn transgenes: 11BT1/2, Cry1ab, GMO5/9, GMO7/8, P35s-cf3/4, and HA-NOS118f/r. In order to determine whether the tortilla chips contained GMOs a DNA extraction was performed and the purification and concentration of each DNA sample was confirmed via a Nanodrop 2000. We performed amplification via PCR using established oligonucleotide primer pairs for the *Zein* gene, which is present in all corn, and upon completion executed an agarose gel electrophoresis. Samples were assayed for expression of the *Cry1Ab* proteins, via ELISA as further evidence of any genetic modification. Since detailed information on the existence of GMOs in food served in restaurants is now legally mandated the findings of this experiment should provide consumers with the information they need to make an informed decision.

117 - The effect of micropylar endosperm on early embryo development

Dongfang Wang

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Proper seed development requires coordinated growth among the three genetically distinct components, the embryo, the endosperm, and the seed coat. This growth coordination is partly achieved through the interaction between the embryo and the surrounding endosperm. Like many angiosperms, Arabidopsis has a nuclear type endosperm. During the initial syncytial stage, the endosperm differentiates into three functional domains: micropylar, peripheral, and chalazal domains. The subsequent endosperm cellularization requires the Fertilization-Independent Seed (FIS)-Polycomb Repressive Complex 2 (PRC2). After endosperm cellularization, the endosperm ceases to grow and is eventually absorbed by the embryo. We discovered two putative invertase inhibitors (InvINH1 and InvINH2) that are involved in the acceleration of embryo growth after endosperm cellularization. InvINH1 and InvINH2 are preferentially expressed in the micropylar endosperm that surrounds the embryo. After endosperm cellularization, InvINH1 and InvINH2 are down regulated in a FIS-PRC2-dependent manner. We hypothesized that FIS-PRC2 complex represses InvINH1 and InvINH2 to increase invertase activity around the embryo, making more hexose available to support the accelerated embryo growth after endosperm cellularization. In support of our hypothesis, embryo growth was delayed in transgenic lines that ectopically expressed InvINH1 in the cellularized endosperm. We also discovered a group of transcription factors as the regulatory connection between the FIS-PRC2 complex and InvINH1. Our data suggested a novel mechanism for the FIS2-PRC2 complex to control embryo growth rate via the regulation of invertase activity in the micropylar endosperm.

118 - The effect of FGF21 on superoxide dismutase levels in myocardium of Ciona intestinalis

Emily McConnell, Heather Evans Anderson

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Cardiovascular disease is the major cause of death in the United States. A primary inducer to this disease is oxidative stress. Oxidative stress is produced in the body when the formation of reactive oxygen species (ROS) exceeds the store of antioxidants, causing an imbalance of oxidants over antioxidants. Oxidative stress destroys macromolecules within cells and can have detrimental effects to the body. The presence of oxidative stress in the myocardium of the heart causes arrhythmias, necrosis, and ventricular dysfunction. Cells have several defense mechanisms that prevent oxidative damage, including antioxidants and enzymes such as superoxide disumtase (SOD). Fibroblast growth factor 21 (FGF21) has many roles in cardiac cells and has been shown to promote mesoderm induction and pre-cardiac specification as well as chamber-specific differentiation, proliferation, and cardiac morphogenesis. In addition, FGF21 can influence rate of SOD production in cardiac cells. The purpose of this study was to investigate if FGF21 promotes SOD activity in the myocardium of a simple chordate model system, Ciona intestinalis. Ciona's cellular simplicity and their close evolutionary relationship to vertebrates makes it a useful model system. Injured and control Ciona hearts were treated with FGF21 and SOD levels were assayed. The results demonstrate that there is a statistically significant difference in SOD level between the injured hearts treated with FGF21 versus controls. Since SOD activity is correlated to oxidative stress levels in cells, results suggest that FGF21 treatment can decrease levels of oxidative stress in Ciona hearts. Future studies include SOD assays comparing treatment with other FGF family members.

119 - Altered developmental toxicity of apple snail egg extracts from two different species and the effects of filtration and temperature to embryos of Xenopus laevis

Andrew Shirley, Johnny Ubi, Ansley Winter, George Cline, Lori Tolley-Jordan, James Rayburn

Jacksonville State University, Jacksonville, AL

Giant Apple Snails (*Pomacea maculata*) are large aquatic snails in the family Ampularidae and considered one of the most detrimental invasive species in the world. Once a population has infiltrated a suitable environment, they are difficult to remove. In the US *P. maculata*

is potentially reducing the population of the native Florida apple snail (*Pomacea paludosa*). *P. maculata* eggs contain an ovorubin protein that gives them a bright pink pigment, protects developing embryos from harsh environments, and has been shown to have neurotoxic effects on mice. It is possible that this neurotoxin is novel to these environments and may have developmental affects on developing aquatic organisms. To test this, we tested the developmental toxicity of apple snail egg extracts (ASEE) to *Xenopus laevis* using standardized FETAX procedures. ASEE was created by homogenizing *P. maculata* and *P. paludosa* egg cases, centrifuging at 3000 RPM for 30 minutes, removal of supernatant (i.e. ASEE). ASEE from *P. maculata* was filtered through a cation exchange column and exposed to 24oC for 2,4,6 and 8 days. Xenopus embryos were exposed to test solutions in petri dishes of various concentrations. For each experiment, 4 controls and 2 replicates of each concentration were measured. Three experiments were performed for each treatment. We measured Mortality, Malformation and embryo length. LC50, EC50 and MCIG were calculated where possible. The results indicated ASEE for *P. maculata* was the most toxic followed by 2, 4, 6 and 8 day exposure to 24°C followed by filtered *P. maculata* ASEE followed by ASEE from *P. paludosa*. These results indicate that there is a novel toxin being exposed in the environment from *P. maculata* (*P. Paludosa* compared to *P. maculata*). Because toxicity is reduced by both filtration and by exposure to 24°C over time, this indicates the toxin is a protein.

120 - Developmental Biology of Zebrafish and Integration of Transgenic Lines to Study Microglia in perspective of Glioblastoma

Anabelle O'Keefe[1,2], Katherine Mccartney[3,4], Umasai Kandepu[2,5], Surendra Rajpurohit[2]

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Glioblastoma is a vicious cancer of the brain that is extremely invasive. Although glioblastomas are primarily found in the brain. We aim to use zebrafish as an organismal model to study how the microglial cells interact with glioblastoma. To achieve this, we are developing the *in-vivo* transparent transgenic zebrafish modeling system to study the microglia function and manipulation during the adverse condition such as inflammation as well as glioblastoma. Microglia are the resident macrophages found in zebrafish and humans located along the central nervous system in the brain and spinal cord. These cells act as macrophages, which support the immune system by cleaning any foreign debris. Zebrafish have become important models for scientific studies because of their affordable maintenance, transparent body plan during the embryo and larval stages, and genomic accessibility. The purpose of this study is to create an all-encompassing transgenic and transparent organism that has three genetic lines displayed in its genetic sequence. The Microglia, NF-kB, and Annexin-5 transgenic lines help display which genes in the brain are being activated by the fluorescent protein. Furthermore, the mutant Casper line of zebrafish contributes to the study by integrating a transparent characteristic in adult zebrafish that allows for simpler visualization and observation in the final model. In our current research study, we have generated the individual strains of microglia, Annexin5, NFkB transgenic line as well the Transparent mutant Casper fishes in our facility. In order to obtain the transparent transgenic progeny, we paired the breeder from these strain in the following order: 1-Capser-x-Microglia, 2-Casper-x-Annexin5 and 3-Casper-x-NFkB. These selected breeders are being breeding and getting the F1 generation of the mixed population. By developing this transgenic phenotype, we will be able to develop this model to utilize microglia cells as a way to approach glioblastomas.

121 - Special Walls: Using Immunocytochemistry to Understand Wall Dynamics During Spermatogenesis in Early Land Plants

Renee Lopez-Swalls

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Spermatogenesis in plants that produce motile gametes, like bryophytes and pteridophytes, involves a series of unique morphogenetic changes that profoundly transform the shape, position and internal structure of every organelle. The result is a coiled, streamlined male gamete with minimal cytoplasm and a locomotory apparatus designed to propel the cell toward the female and through the narrow confines of the archegonial neck. Key to this process is the production of unique cell walls that are integral to gamete maturation. While common wall polysaccharides and callose have been detected in scattered taxa, very little is known about the sequence of wall formation and wall composition during sperm cell differentiation in plants that produce swimming sperm. Utilizing histochemical techniques coupled with immunocytochemical localizations with monoclonal antibodies (MAbs), give a detailed survey of cell wall polymer and arabinogalactan protein (AGP) distribution during male gametogenesis in the moss, *Aulacomnium palustre*, and the fern, *Ceratopteris richardii*, both key taxa in land plant phylogeny. Although the sequence of wall layers produced during spermatogenesis in *Aulacomnium* resembles that of *Ceratopteris,* the wall constituents are remarkably different in the two plants. Most notable is the abundance of hemicelluloses and the absence of callose in the spermatid walls of *Aulacomnium*. Another key finding is that although AGPs are abundant in the extraprotoplasmic matrix of developing sperm cells in both plants, AGPs are expressed in the remaining walls of *Aulacomnium* spermatids but not *Ceratopteris*. The results of this study advance significantly our understanding of cell wall dynamics during spermatogenesis in early land plants.

122 - Impacts of cogongrass (Imperata cylindrica (L.) Beauv.) on arthropod community structure in native Black Belt Prairie

William Pettis, Kevin Morse, John McCall, Lee Stanton

University of West Alabama, Livingston, AL

Cogongrass (*Imperata cylindrica*), a perennial C4 grass, is invasive in many parts of the world including the Southeastern United States. Studies have demonstrated the negative impacts of this invasive grass on native ecosystems, but few have investigated how cogongrass affects arthropod abundance and diversity. As such, we compared arthropod communities in native Black Belt Prairie to areas of the prairie infested with monostands of cogongrass. Using sweep nets and pitfall traps, samples were collected during June, July and August 2019, and resulted in the collection of approximately 3000 individuals representing nearly 200 taxa. Preliminary data suggest that these

invasions are shifting arthropod community structure at both the ground and canopy levels. It appears that insect specialists and those sensitive to environmental shifts (tiger beetles (Cicindelidae), weevils (Curculionidae), and certain planthoppers (Fulgoroidea)) are either absent or rarely found in cogongrass dominated areas. In contrast, we found the diversity and abundance of others increased at the ground level in monostands of cogongrass (beetles (Carabidae and Elateridae)). Although more research is needed, shifts in arthropod community structure in the wake of cogongrass invasions have the potential to reduce host-specific species, pollinator diversity, and ultimately affect how energy is transformed in these environs.

123 - Using a community occupancy model to estimate forest bird habitat relationships in eastern Virginia and North Carolina

Nicholas Flanders, Lytton John Musselman, Eric Walters

Old Dominion University, Norfolk, VA

Forests in the southeastern United States (US) provide critical habitat in winter for a variety of avian species, many of which are migratory and frugivorous. Relationships between winter occurrence and specific forested habitat types are poorly known for many forest bird species in the region. Given the critical role of frugivorous birds in maintaining populations of plants beneficial to a variety of wildlife species, information on habitat requirements of these avian species are of special interest to land managers. Stratified random sampling was used to select 96 circular plots with 25-m radii to repeatedly survey for the presence or absence of avian species. These plots were in the Coastal Plain and Piedmont regions of Virginia and North Carolina, with approximately one half of the plots in forested wetlands and remaining plots in forested uplands. Plots were sampled in winters (Dec-Mar) 2015-2019. We detected the presence of 58 forest bird species and analyzed occurrence data using a community occupancy model to estimate species-specific relationships between forested habitat type and occupancy while accounting for the imperfect detection of species. We found significantly positive relationships between forested wetland habitat and occupancy for five species including the rusty blackbird (*Euphagus carolinus*), a species of conservation concern, and two other frugivores: gray catbird (*Dumetella carolinensis*) and yellow-rumped warbler (*Setophaga coronata*). Significantly negative relationships between forested wetland habitat and occupancy were estimated for three avian species including the locally uncommon red-headed woodpecker (*Melanerpes erythrocephalus*). Detection rates were highly variable across species and extremely low for some species, emphasizing the need to account for imperfect detection when estimating habitat relationships and comparing occupancy rates across forest bird species wintering in the southeastern US.

124 - Using microsatellite markers to compare genetic population structure between rainbow trout (Oncorhynchus mykiss) and brown trout (Salmo trutta) downstream of the Buford Dam on the Chattahoochee River, Georgia

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Rainbow and brown trout have been stocked in the Chattahoochee River since the 1960s. Brown trout stocking was terminated in 2006 due to sustained natural reproduction. Conversely, the rainbow trout cannot sustain viable populations naturally due to environmental conditions not conducive for reproductive success. Eventually routine stocking may lead to reduction in genetic diversity. In this study, 41 rainbow trout and 33 brown trout species were compared genetically through use of microsatellite markers. Samples were obtained from three zones downstream of Buford Dam and the GA-DNR Buford Trout Hatchery to serve as a control group in genetic analysis. Species were analyzed using 11 fluorescently labeled microsatellite primers on previously extracted DNA. Microsatellite frequencies and population structure were compared within and between species as well as across zones. Our analysis will aid determination of whether variations in stocking activity on the Chattahoochee have played a role in genetic variation and reproductive successes of these species.

125 - Canopy Assessment & Niche Modeling of Microstegium vimineum (Trin.) A. Camus in Central Appalachia

Nick Koenig, Jennifer Koslow

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Invasive species are a threat to native plant diversity. *Microstegium vimineum* (Japanese Stiltgrass) is a shade tolerant grass native to South and East Asia that has invaded much of the eastern United States. Although some researchers expect that intact biological systems will resist invasions by novel species, natural disturbances such as treefall gaps still provide openings in these communities. We observed that *M. vimineum* appeared to be more abundant in light gaps in Lilley Cornett Woods, an old-growth forest in southeastern Kentucky. We visited 41 patches of *M. vimineum* and estimated its percent coverage in 4m x 4m plots. We also used hemispherical photography to determine the percent canopy openness in these locations. Finally, in 14 plots, we also removed *M. vimineum* to determine the plot-level biomass as a check on our coverage estimates and to help manage this invasive species. We ran three linear regressions to assess relationships among the three variables. There was no relationship between canopy openness and either percent coverage or biomass. Percent coverage and biomass had a strong positive relationship. From this, the data supports the statement that *M. vimineum* is a shade tolerant species when growing in an old-growth forest, which intensifies the need for removal. We also used the program MaxEnt, a niche modeling service, to model the distribution of *M. vimineum* in the northeastern United States. These models give insight for management practices, probability distribution maps, and predicted density of growth for *M. vimineum*.

126 - Evaluation of machine learning methods to model species distribution and habitat suitability of American ginseng (Panax quinquefolius) in Virginia

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American ginseng (*Panax quinquefolius*) is a well-known and sought-after medicinal plant native to North America that is facing increased threat of extinction due to overharvesting, herbivory, and habitat loss. Species distribution and habitat suitability models may be valuable to landowners interested in sustainable harvest or to institutions interested in the conservation and restoration of the species. With unequal sampling efforts across a region of interest, it is likely that some locations with appropriate habitat may be misrepresented in model predictions. This study refined a state-derived species distribution model for ginseng through increased sampling effort across the Cumberland Plateau of Virginia and experimental manipulation of model parameters using the machine learning method Random Forest. Through many iterations, sixteen final models were constructed with various parameters such as spatial partitioning, removal of correlated variables, and limiting the spatial extent for background point generation in an effort to reduce overfitting and increase accuracy. Models were evaluated using partial dependence plots, area under the curve (AUC), and out-of-bag error (OOB error). Of those models, this study determined that various methods may be used depending on the goal of the project—resulting in more accurate and realistic species distribution and habitat suitability models than were previously available. This study concludes that, although various model parameters can be altered to change the product thereby increasing accuracy or reducing overfitting, the most effective means of reducing the impact of sampling deficiency is to balance sampling effort across the region of study.

127 - Modeling Relationships Between Host Fish Availability and the Reproductive Success of Mussels

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The diverse community of North American freshwater mussels are declining rapidly; nearly 70 percent are considered extinct or imperiled due to water pollution and dams. Mussels act as a keystone species in determining water quality by continuously filtering out algae, bacteria, and other organic and inorganic matter from the water column as they feed. Undigested material is expelled from the mussel as pseudo-feces and inorganic materials are held in a matrix which reduces their resuspension.. This pseudo-feces is a food source for many other invertebrates. Mussels and fish exhibit a parasitic relationship requiring each mussel species to have a specific fish host to complete their life cycle. A binomial probability model was developed using the freshwater mussel population native to the Ohio River to facilitate investigation of the correlation between host fish availability and the reproductive success of mussels. The model assumes two possible outcomes; one in which the host fish comes in contact with the mussel, defined by the visibility radius, and the other when it does not. Twenty sites were randomly chosen and sampled using electrofishing for 48 different fish species by the Ohio River Valley Water Sanitation Commission (ORSANCO). A subset of nineteen sites were also sampled for 23 mussel species over six perpendicular 100 meter transect lines using SCUBA. The probability model predicts the effects of change in host fish availability and the visibility in the river on the overall reproductive success of mussels.

128 - Habitat Utilization and Impact of Flooding on James spinymussel (Parvaspina collina) Populations in Virginia Streams

Christine Verdream, Dr. Christine May

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The James spinymussel (*Parvaspina collina*), is one of many endangered freshwater mussels found in Virginia and results from this project will provide information that can be applied to recovery plans for mussels by identifying high survival habitats. The primary objective of this study was to investigate the relationship between flood disturbance and population dynamics of co-occuring *P. collina* and *V. constricta* in a flood prone stream and compare to a stream below a dam that dampens flood disturbance. A second objective was to identify habitat preferences of *P. collina* in both streams. Analyses used long-term mark-recapture data sets for two sites in the James River watershed, as well as habitat data collected from both sites including substrate, depth and velocity measurements collected during summer low-flow conditions. We hypothesized that the populations in the flood prone stream would exhibit unstable population dynamics due to the lack or refugia in the predominantly sand-bedded channel. Results thus far support this hypothesis, with emigration increasing as discharge increases and recapture probability decreasing following high flow events. In addition, it was hypothesized that mussels will utilize habitat patches within the streambed that contain coarser grained substrate, in conjunction with lower depths and velocities. Preliminary analyses suggest that many mussels in the flood prone stream are transiently occupying unstable habitats, often in areas predominantly comprised of sand. Understanding where mussels are most likely to survive and reproduce it crucial for identifying potential habitat and determining where propagated mussels should be released.

129 - Effects of Sex and Body Size on Parasite Load in Western Mosquitofish

Megan Gibbons

Birmingham-Southern College, Birmingham, AL

Parasite load results from complex interactions that can include the sex and body size of the host. Studies suggest that male-biased parasitism is more common that female-biased parasitism, possibly because males tend to have weaker immune systems than females. Additionally, host body size typically has a positive correlation with parasite load, as larger hosts a) provide a larger habitat, 2) are typically older, suggesting that they have had more time to accumulate parasites, and 3) may have the ability to travel further distances than smaller hosts, exposing them to a greater diversity and number of parasites. Western mosquitofish, *Gambusia affinis,* are often infected with the trematode, *Uvulifer ambloplitis*,that causes Black Spot Disease (BSD). Female *G. affinis* have a larger average body size than males,

so based on prior research, it was unclear whether males or females would have a greater trematode load. In this study, we examined the relationship between sex and body size on number of BSD spots in *G. affinis*. We found that body size was positively related to parasite load and that females had a greater overall parasitic load than males. We also determined that females had a stronger relationship between body size and number of spots than males, possibly due to unique metabolic costs that may impact their immunity.

130 - Effects of the Eastern Continental Divide on Gene Flow between Populations of Freshwater Fish

Reginald Turner, James E Russell

Georgia Gwinnett College, Lawrenceville, GA

Georgia is bisected by the southeastern continental divide that separates water flowing to the Gulf of Mexico and water flowing to the Atlantic Ocean. How do animals navigate the divide and the obstacles within distinct watersheds? In cooperation with the Gwinnett County Department of Parks and Recreation and other regional partners, we have developed a research program investigating the effect of the continental divide on fish species to test hypotheses related to gene flow within and between watersheds. Since the continental divide acts as a barrier to water flow, separating river watersheds, our initial hypothesis was that the continental divide also acts as a barrier to gene flow for species restricted to aquatic habitats. Using a paired-sample design, headwater stream fish communities either side of the continental divide have been, and are continuing to be, sampled. Dominant species found in these communities are in the genera *Semotilus*, *Nocomis,* and *Campostoma*. Tissue samples taken from the caudal fins of collected stream fishes were used for molecular phylogenetic analyses using mitochondrial and nuclear gene regions. Preliminary sequencing results of select gene loci have given some support to the continental divide gene flow hypothesis. However, nuclear and mitochondrial data sets are not entirely congruent. Mitochondrial phylogenetic patterns for *Nocomis leptocephalus* (Blue head chub) indicate gene flow within the Chattahoochee watershed may be more restricted than between watersheds across the continental divide. Whether these results represent a speciation event for *N. leptocephalus* or a geographic range expansion of a related sub-species is currently being investigated with expanded sampling and molecular analyses.

131 - Microbial assemblages in association with crayfish ectosymbionts

Kaleb M. Bohrnstedt, Matthew M. Cooke, Nathan Edmondson, Luke T. Fischer, Mark Fischer, Gabriel Hooper, John Hoverson, Thomas A. Keplar, Matthew Becker, Kyle J. Harris

Liberty University, Lynchburg, VA

Crayfish are known to benefit from branchiobdellidan worms as these worms consume bacteria on crayfish gills, providing a cleaning symbiosis. In our first experiment, we inoculated crayfish with four branchiobdellidans and others had all branchiobdellidans removed. It was expected that the presence of worms would decrease the amount of bacteria in the gill chamber, thus allowing an increase in both growth rates and dissolved oxygen (DO) uptake. Crayfish were then observed for DO uptake and microbial swabs were collected to identify colony forming units (CFUs/g crayfish). Our hypothesis was that the branchiobdellidan presence would result in increased DO uptake due to the cleaning effect of the worms on the gills. Based on the results from this study, we then collected microbial swabs of crayfish and environment from a nearby freshwater stream. DNA was extracted from the microbial swabs and the 16S gene was amplified for DNA sequencing. Sequenced microbes were then compared to stream order, stream environment (water and substrate), and the number of branchiobdellidan worms present on the crayfish. From the tank study, the observed percent change in blotted wet mass (BWM) over eight weeks showed that the control crayfish group grew 26.2% more than the experimental group (with four worms/crayfish). No significant difference was found in the mean DO consumption between control (0.094 mg/l/g*2hr) and experimental (0.090 mg/l/g*2hr) groups. A gill chamber bacterial analysis and characterization showed that the logged mean number of colony forming units/gram crayfish (log10 CFUs/g) was greater for the experimental group (3.80 log10 CFUs/g) than the control group (2.84 log10 CFUs/g). The bacteria identified revealed two unique microbial assemblages. From the field-based study, Qiime2 analysis of the raw sequencing data from crayfish with (N=19) and without(N=14) branchiobdellidans revealed differences in alpha diversity. However, the limited sample size warrants further investigation.

132 - A preliminary assessment of Hg and MeHg bioaccumulation in Subarctic wetland food webs

C. Kabryn Mattison[1], Blake R. Hossack[2], LeeAnn Fishback[3], Kelly L. Smalling[4], Collin A. Eagles-Smith[5], Jon Davenport[1]

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Northern latitudes are warming at a rate twice that of the global average. This warming is melting permafrost in many areas, causing the release of stored mercury (Hg) which can become methylated into neurotoxic methyl-mercury (MeHg). Release of mercury into Arctic and Subarctic ecosystems suggests the possibility of bioaccumulation up the food web to humans. To date, there are limited records of Hg accumulation in the Subarctic region. To investigate potential mercury bioaccumulation of MeHg in the Subarctic, we collected sediment and animal tissues from wetland ecosystems of the Hudson Bay lowlands near Churchill, Manitoba and analyzed them for MeHg and total Hg (THg). We collected tissue samples from Wood frog (*Rana sylvatica)* embryos and larvae, Boreal Chorus frog (*Pseudacris maculata)* larvae, and Stickleback fish (*Pungitius pungitius & Culaea inconstans*). We hypothesized that MeHg would be present in all species, but in higher concentrations at higher trophic levels. We found that MeHg in Wood frog larvae was strongly correlated with MeHg of Boreal chorus frog larvae in the same wetlands. Both species of Stickleback fish had the highest levels of MeHg. The highest two values of MeHg in tadpole tissues were from two thermokarst (i.e. melting permafrost) wetlands. Additional samples were taken in summer 2019 to test additional habitat types and expand our samples. Our study is the first to measure baseline levels of Hg in amphibians in the subarctic, so future research can build upon our foundational data to track changes in Hg through time.

133 - Stream Impoundment Impacts the Life History Traits of Bluegill (Lepomis machrochirus)

Thomas Bustamante, Bradley Lamphere

University of Mary Washington, Fredericksburg, VA

Human alterations on natural habitats create selective pressures that can lead to evolutionary change. Stream impoundment causes stream ecosystems to rapidly transform into lentic environments, creating novel selection pressures on the resident fish. Life history traits, such as gonad mass and size at maturity, are often sensitive to changes in environmental conditions. To better understand how natural populations respond to stream impoundment, we measured whether gonad mass and size at maturity in Bluegill were different between reservoirs and streams. Overall, males from streams had larger gonads and matured at a larger size than males from reservoirs. In contrast, gonad mass and size at maturity of females did not differ between habitats. The sex-bias and direction of the differences are consistent with the divergence between lake and stream life histories being attributed to sexual selection as opposed to predation pressure. These results illustrate the potential for a widespread human impact, such as stream impoundment, to alter the phenotypes of fish populations living in these ecosystems.

134 - Unionid bivalves in the Greenup Pool of the Ohio River

Jacob Miller

Marshall University, Hurricane, WV

Unionid bivalves- or, freshwater mussels- are at the foundation of freshwater communities and ecosystems serving as a natural water filter and food source for many species. However, anthropogenic activity in the last century has had a severe negative impact on freshwater mussel diversity and abundance. Freshwater mussels comprise more of the federally threatened and endangered species list than any other taxonomic group. The status of freshwater mussels and the impacts they face raises concern across much of the US and, on a more personal level, the Greenup pool of the Ohio River. I am interested in further understanding the status of freshwater mussels in the Greenup pool and hope to answer some questions through a survey of 20 randomized sites by qualitative SCUBA. Freshwater mussels will be collected and identified to investigate species diversity and abundance. An undetermined number of sites will also be excavated for juvenile mussels that are buried in the substrate to determine if and what species are reproducing in the Greenup pool. This data will be compared to electrofishing data from the Ohio River Sanitation Commission (ORSANCO) as well as data from a similar project completed in 2016. With this project we are hoping to see if there is a relationship between the freshwater mussel species presence and their corresponding host-fish species presence. We are also interested in determining how many random sites are needed to characterize a pool in large river systems. With the comparison of data from this project and projects from recent years we will be able to contribute to the construction of a protocol for big river mussel surveys.

135 - Pollution Tolerance of Crayfish Ectosymbionts

Kyle J. Harris, Megan Pizzo, Zachary Youngbar

Liberty University, Lynchburg, VA

In the natural environment, it is common for pesticides to be pulled into neighboring bodies of water due to runoff. When pesticides are introduced into these rivers or lakes, they are provided the opportunity to come in contact with non-target organisms. Macroinvertebrates are commonly used to study pollution tolerance in aquatic ecosystems. In previous studies, the effect of pesticides on crayfish was explored through chronically exposing crayfish to low concentrations of Atrazine (ATZ). Significant tissue degradation observed in the hepatopancreas tissue of the crayfish indicated sub-lethal effects in the freshwater invertebrate.

Although the effect of pesticides on macroinvertebtrates has been studied, it is relatively unknown how common pollutants (e.g. pesticides from runoff) impact symbiotic relationships. In this study, two of the most commonly applied pesticides from agricultural practices which make their way into streams, Glyphosate(GLY) and Atrazine, are examined for effects on crayfish ectosymbionts (Branchiobdellidan worms). Branchiobdellidan worms (BW) were exposed to ATZ and GLY at 50 and 500ppb over 48-hours. ATZ and GLY did not result in mortality when exposed as a single pollutant at 50 and 500ppb. Interestingly, the combined effect of ATZ and GLY at 50 and 500ppb resulted in 100% mortality after 48-hours. The results indicate that BW can survive the potential lethal effects of single pesticides which enter freshwater systems. Yet the more relevant joint pesticide acute exposure on BW indicates a low pollution tolerance which could lead to mortality or displacement of these crayfish epibionts in freshwater ecosystems. Though lethality was not observed in individual treatments, sub-lethal tissue degradation effects were identified at 50ppb from the GLY treatment. These findings indicate that introduction of common pesticides at environmentally relevant doses into freshwater ecosystems can have lethal and damaging sub-lethal effects on annelid ectosymbionts and potentially their role as a cleaning symbiont within freshwater ecosystems.

136 - Analyzing Extinction Risk in Local Arthropods: A Phylogenetic Approach

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Global biodiversity loss is accelerating rapidly across all major taxa, but some species are more susceptible to extinction than others. What makes a species more or less susceptible to extinction may lie within its evolutionary past and current ecological traits. In order to best conserve high-risk species, we must therefore understand which traits are most influential to extinction risk for certain species within specific environments. Analyses of extinction risk in terrestrial arthropods are scarce, so we used a trait-based approach to assess the effect of initial abundance and if any morphological, behavioral, life-history, and feeding-related traits were associated with the extinction of local arthropods in response to experimentally simulated habitat loss. We found that the most influential factor in a species' extinction was

its initial abundance before habitat loss was implemented, which supports the idea that rare species are more susceptible to extinction than common species and that stochastic factors may override trait-based factors. Although a species' initial abundance will not always reveal its risk of extinction, conservation prioritization should focus on terrestrial arthropod species with low abundances.

137 - Low abundance of three tick species in the Piedmont of North Carolina

Madeline Seagle, Maximilian Vierling, Kevin Smith

Davidson College, Davidson, NC

Multiple species of ticks, including *Ixodes scapularis*, *Amblyomma americanum*, and *Dermacentor variabilis* occur in high and increasing abundance in both the northeast and southeast United States. North Carolina is at the nexus of spread of these species, with high occurrence and abundance of *I. scapularis* to the north and *A. americanum* to the south. Despite this, there are few records of these species in the Piedmont of North Carolina, including the greater Charlotte metropolitan area. Here, we update the known occurrence and abundance of these species in the North Carolina Piedmont. We surveyed for ticks using cloth drags, CO_2 traps, and leaf litter samples at a total of 79 sites across Mecklenburg Co., South Mountains State Park, Stone Mountain State Park, Duke Forest, and Morrow Mountain State Park, all in North Carolina, during the summer and fall seasons of 2019. From these surveys, we had only twenty tick captures, illuminating the surprisingly low abundance of ticks in North Carolina. Our results indicate the possibility of underlying habitat and host factors that prevent North Carolina from experiencing as high of tick abundances as states to its north and south.

138 - Forensic Entomology: The Case of the $25,000,000 Ant Colony

Ed Mondor

Georgia Southern University, Statesboro, GA

Insect evidence is playing an increasingly pivotal role in civil trials. For example, insects often feature prominently in food contamination and structural defect cases. In this talk, I will describe my role as an expert witness in a personal injury civil action (*Shanta Greene v. The Mayor and Aldermen of the City of Savannah - Civil Action File No.: STCV1200532*). In this case, the plaintiff was crushed by a falling Live Oak tree limb while riding in a vehicle on a city street. In addition to the tree limb, hundreds of large, black ants were observed crawling on the damaged vehicle. As a result of being impaled by the tree limb, the plaintiff lost her right leg, part of her pelvis, suffered a brain injury, and is relegated to a wheelchair. I was hired by the plaintiff's attorneys to determine the ant species present on the vehicle and to give an expert opinion as to whether this species in any way contributed to the tree limb failure. Here I will describe the methodology used to determine the ant species in question, and what this ant species indicated about the general health of the tree that shed the limb. In sum, this talk will provide a better understanding of the role a forensic entomologist plays in a civil investigation and trial.

139 - Prevalence of the parasite pathogens that cause Lyme disease in Southwestern Georgia and Southeastern Alabama.

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The occurrence of Lyme disease is on the rise in the United States. Lyme disease is caused by infection from the *Borrelia burgdorferi* bacteria. The bacteria are spread through the bite of the black-legged deer tick, *Ixodes scapularis.* At present, the majority of cases of Lyme disease are located in the Northeastern United States. The lack of prevalence in the southeastern United States has been attributed to variations in habitat. However, several cases of Lyme disease in the Southeastern United States have been misdiagnosed. The prevalence of *Borrelia burgdorferi* in Southwest Georgia and Southeastern Alabama has not been addressed. We collected 165 ticks in December 2018 and 2019 in Southwest Georgia and assessed the presence of *Borrelia burgdoferi s.s.* through real-time PCR methods. Of the 41 sampled to date, one of them tested positive for *Borrelia*, although not *B. burgdorferi.* Further research will include sampling the other 124 ticks for the presence of this bacteria. Possible explanations for such a low occurrence may include the presence of antibacterial properties of deer blood, as well as dry conditions due to large amounts of pine forests in the region. These may hinder the amount of biting ticks, therefore the occurrence of Lyme disease.

140 - Light preference for night active insects

Jazlyn Pointer

Uuniversity of North Carolina at Pembroke, Pembroke, NC

While fluorescent bulbs are commonly used for illumination, many insects are attracted to the light emitted. Numerous experiments have shown that nocturnal insects are most attracted to lights that emit large amounts of ultraviolet radiation, such as fluorescent light bulbs. Insects are also attracted to black lights and are often used by entomologists as light traps. While both lights are known attractants, it has not been fully explored if they both attract the same type or quantity of insects. For this comparison, two white sheets were hung in an area with minimal light pollution. Each sheet had either a black light or fluorescent light angled toward the sheet for one hour. Insects were then collected by hand, aspirator, or net. Sampling took place once every month for the fall and spring. The insects were preserved and identified to species. Preliminary results show that Hemipterans, mainly cicadas and stink bugs, were more attracted to the black light while dipterans were more attracted to the fluorescent light.

141 - The Richness and Abundance of Bacteria in the Foregut, Midgut, and Hindgut of the Brown Panopoda (Panopoda carneicosta) and the Curved Ribbon (Dinumma deponens)

Kathryn Petty

Birmingham-Southern College, Birmingham, AL

The gut microbiome of adult moths and butterflies have not been widely researched, but research has been done on the guts of crop pest caterpillars. As the primary location of digestion in caterpillars is the midgut, much research has been done on it. As far as the other two gut sections are concerned, little work has been done on them. Since both the foregut/crop and the hindgut have been understudied, this study revolves around them as well as the midgut. It also is focused on the adult moths since so little is known about their digestion. The question that is being asked is whether the abundance and richness of culturable bacteria differs in the three gut sections (foregut/crop, midgut, and hindgut), given the differences in pH of the alkaline midgut and relatively neutral fore- and hindgut, of two different species from the Erebidae family, *Panopoda carneicosta* and *Dinumma deponens.* Four individuals of *P. carneicosta* and seven individuals of *D. deponens* were captured from mixed pine-hardwood second-growth forests in Birmingham, AL during June and July of 2019. These individuals were dissected, and their gut sections were processed to determine what culturable bacteria was in each section. This process resulted in forty-one morphospecies of bacteria, only sixteen of which were able to be sequenced given the primers used. These bacteria were statistically significant in abundance and richness for each gut section per species in *P. carneicosta* but not in *D. deponens.* The two species showed differing results as *P. carneicosta* had a richer and more abundant set of bacteria in the midgut, but *D. deponens* had more richness and abundance shown in the hindgut. This may mean that *D. deponens* relies more on its hindgut for bacterial processing while *P. carneicosta* relies more on its midgut.

142 - Get to know your new neighbor: biology of the introduced brown widow spider

J. Scott Harrison

Georgia Southern University, Statesboro, GA

Introduced species often generate ecological and economic costs. These species can also serve as interesting natural experiments as they are often exposed to new ecological conditions, undergo dramatic fluctuations in population size, and produce offspring that are interpopulation hybrids. The brown widow spider (*Latrodectus geometricus)* is thought to be native to South America or Southern Africa, but its distribution has expanded to most continents by human introduction. In the continental USA, *L. geometricus* was first documented in south Florida in the 1930s, but since the early 2000s has become abundant in northern Florida, Georgia, South Carolina, Alabama, Mississippi, Louisiana, Texas, and southern California. This species is commonly found around urban structures including shopping centers, homes, parks, and landscaping areas. In this talk, I will summarize research on the evolutionary ecology and population dynamics of brown widows in the context of its propensity to establish introduced populations. Our findings show that the distribution of genetic variation in southeastern US populations is consistent with multiple introductions. In addition, inbreeding depression is significant when mating occurs between related individuals, indicating that inbreeding has been avoided during the introduction and that local dispersal mechanisms allow for inbreeding avoidance. Finally, bacterial endosymbionts are common but seem to only have minor impacts on the reproductive biology and ecology of this species.

143 - Phytoextraction of Pb contaminated soils using soil chemical manipulation and hormone enhancement of Panicum virgatum L

Austin Gilly

Kennesaw State University, Roswell, GA

This study is aimed at evaluating phytoextraction methods by growing switchgrass under foliar application of growth hormones and subjecting them to a chelate solution to access if there would be a significant increase in uptake of Pb in contaminated soils. Plants were subjected to the following treatments: (1) control Infuse (CI), (2) control [Infuse and NTA solution (CN)], (3) [NTA/Infuse/Salicylic acid (SA)], (4) [NTA/Infuse/BAP (BAP)]. Pots were filled with Pb contaminated soil and then seeded. Plants were watered with 200 mil of nutrient solution twice a week for the experiment. Foliar application of the plant growth hormones salicylic acid and 6-Benzyladenine (BAP) was applied with hand spray bottles twice a week for target plants. After 6 months of growth, a 2 ppm solution of Infuse was applied regularly for 2 weeks by 100 ml solution. Infuse treatment continued for the CI plants and the Application of the NTA solution was applied three times a week for 40 days till plants showed severe heavy metal toxicity for all other treatments. After plants showed clear symptoms of metal toxicity the switchgrass was cleaned without damaging plants. Plants were labeled and dried at 65 C° for a week and dry mass was recorded. Plants were then placed individually in digestion tubes and ran through the Kennesaw State University ICP-MS for Pb, Fe, and Al concentrations. Difference in dry weight between treatments were only significant between SA and CI samples. The BAP compared to SA dry weight was close to significant with .07 confidence. The BAP and CN treatments had significantly less dead leaves than live while the SA and CI treatments had about an equal amount suggesting a higher concentration of metals in the SA and CI plants.

144 - Update on the distribution of Rhododendron eastmanii (May-white azalea, Ericaceae) in South Carolina

Charles Horn

Newberry College, Newberry, SC

Rhododendron eastmanii (May-white azalea) was first described in 1999 and at that time was known from only two locations in South Carolina. In the subsequent 20 years, much field work has resulted in the documentation of 62 populations in 13 counties, all within South Carolina. Recent work has emphasized revisitation of populations within the Sumter National Forest to assess the status of previously populations, some not visited since 2000. Additionally, attempts to fill in distributional details along the Congaree Bluffs area of Calhoun

and Orangeburg counties has continued. During field trips, more accurate population surveys have been completed to document population size, geographical range, and reproductive success. Most individuals are found on slopes of ravines at stream headwaters. As expected, some populations have declined, and some have expanded. Invasive species are apparently becoming more common and are negatively impacting azaleas, especially *Lonicera japonica*, and *Elaeagnus umbellata*. On a positive note, surveys of ravines adjacent to known populations have been fruitful in locating additional plants.

145 - Comparing floristic biodiversity of power line cuts to adjacent forest habitats in Hamilton and Marion Counties, Tennessee; Dekalb County, Alabama; and Walker County, Georgia

Megon Stepaniuk

University of Tennesee at Chattanooga, Chattanooga, TN

Southeastern grasslands are open areas with little to no trees that are dominated by native heliophytic forbs and grasses. Over time, they have disappeared for various reasons, such as conversion to farmlands, tree encroachment, and wildfire suppression. There are many kinds of southeastern grasslands and each of these offers a unique home to different species. As these grasslands are disappearing, so are the organisms that rely on them. It is estimated that frequent extinctions of grassland-dependent organisms will begin by as early as 2050. The focus of this investigation is to compare the flora of power line cuts to their adjacent forest habitats in 1km transects to quantify and directly compare the native biodiversity with open lands and forested areas, especially with respect to conservative species. Three site locations were selected within the Tennessee. One site on Lookout Mountain, GA is on an east facing slope in a residential area leading to many invasive species being present, such as *Lonicera maackii* and *Verbena brasiliensis*. A second site, on Raccoon Mountain, TN is similarly on an east facing slope, though the mountain is owned by TVA and has no residential housing. This contrasts to Lookout Mountain such that there are many native species here like *Trillium cuneatum, Scutellaria ovata,* and *Carex hirsutella*. A third site at Little River Canyon, AL is located further south, and has many conservative species, such as *Sarracenia oerophila, Polygala nana*, and *Cleistes divaricata*. One aim of this effort is to increase awareness about the vast biodiversity of rare grasslands compared to deciduous forests on the Cumberland Plateau, and therefore educate citizens on why we should work to conserve and protect them.

146 - Preliminary Vascular Flora of Walls of Jericho State Natural Area, Franklin County, Tennessee

Nate Parrish, Joey Shaw

University of Tennessee at Chattanooga, Chattanooga, TN

The Walls of Jericho State Natural Area in Franklin County, Tennessee represents an area of unique physiography and high biodiversity within the state. Owing its name to a 300-foot limestone gorge central to the natural area, the surrounding region has an unusually high amount of exposed limestone compared to the majority of the Cumberland Plateau in Tennessee. While not within the scope of this study, the Walls of Jericho is part of a large conservation area that is shared by 26,000ha in Alabama as the Martin-Skyline Wildlife Management Area. The area has been surveyed for rare plant populations in the past but no comprehensive flora of the area has been completed to date. The total study area, consisting of 930 hectares of dissected Cumberland Plateau and Plateau Escarpment, encompasses a wide variety of habitats. Much of the area was selectively logged during latter half of the 20th century, but large portions of land within close proximity to the major creeks running through the natural area and the nearby Bear Hollow Mountain WMA in Tennessee were protected from the majority of the impacts. To date, 32 collection trips and over 500 collections have been made from the area, with at least 175 taxa confirmed from the site so far, encompassing 72 families and 126 genera. Notable taxa found at the site so far *include Viburnum bracteatum* and *Clematis glaucophylla*, both of which are state listed. Despite the area's use history, the documented occurrences and number of invasive species has been relatively low, outside of a select few areas.

147 - Sandmyrtle (Kalmia buxifolia, Ericaceae) biogeographic history supports the Cape Fear Arch as a Glacial Refugium

Emily Gillespie[1], Tesa Madsen-McQueen[2], Torsten Eriksson[3], Allison Welz[1], Zack Murrell[4]

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Sand myrtle, *Kalmia buxifolia* (Bergius) Gift & Kron, exhibits a disjunct distribution in eastern North America, ranging from the NJ Pinelands (NJP) to the Sandhills/Cape Fear Arch (SCFA) and westward into the Southern Appalachian Mountains (SAM), with no present-day geographic connection between NJP and southern populations, and very little between the SAM and SCFA populations. This species exhibits considerable morphological variability, leading experts to recognize between one (current consensus) and three species historically. Here, we update efforts to understand the biogeographic history and genetic structure of this species within the context of southeastern biogeography. We developed microsatellite markers using populations from each of the three regions and then applied these markers to a total of 11 populations of Sand myrtle and its closest relative, *Kalmia procumbens* (L.) Gift, Kron & P. F. Stevens ex Galasso, Banf. & F. Conti and evaluated various measures of population diversity and divergence. We evaluated phylogenetic signal using both chloroplast and nuclear markers and compared this to signals within the microsatellite data. Our updated dataset continues to reveal striking inter-population divergence in the south. Our analyses provides support for the hypothesis that the Cape Fear Arch of the Carolinas was a glacial refugium, from which Sand myrtle migrated northwestward into the SAM and northward into the NJP. Intermittent genetic connectivity between the NJP and SCFA populations appears to have continued for some time, but SAM populations have diverged considerably during the same period, raising new questions about the mechanism of divergence in the mountain populations.

148 - Zephyranthes verecunda Herb. and Z. minuta (Kunth) D. Dietr. (Amaryllidaceae), a puzzle for two centuries

Ray Flagg[1], Gerald Smith[2], Abisaí García-Mendoza[3]

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Herbert described *Zephyranthes verecunda* and *Z. striata* in 1825. In both publications he referred to *Amaryllis minuta* Kunth (1816) as possibly being more related to *Z. striata*. Because of the paucity of specific characters given in Kunth, Herbert found it impossible to decide with certainty if the affinities of *Z. striata* applied to *A. minuta*. Herbert (1837) treated *Z. verecunda* and *Z. striata* as related varieties, and he doubted that *Z. striata* would be able to breed true to "its distinguishing characteristics with certainty when raised by seed." An objective of our studies is to determine the level of relationship between *Z. verecunda* and *Z. striata* by studying field images and taking data from herbarium specimens. Modern taxonomists treat *Z. verecunda* and *Z. minuta* (Kunth) D. Dietr. (1840) as synonymous. After examining the type plate of *Z. verecunda*, the type specimen of *Z. minuta*, making observations and measurements from herbarium specimens and field images of both species, it has become clear to us that we cannot accept the concept that they are synonymous. Overall, *Z. verecunda* tends to be larger than *Z. minuta*, the former having its scape longer, flower bigger, and mature leaves wider than scape.

149 - Molecular Systematics and Taxonomic Implications of Southeastern Amsonia

Destiny Clark, Michael Sandel, Brian Keener

University of West Alabama, Livingston, AL

The genus *Amsonia* (APOCYNACEAE) has long been a source of taxonomic ambiguity in the southeastern United States. Currently, there are ten formally recognized species with an additional infraspecific taxon. Several other taxa have been described but later sunken into synonymy. There have been various attempts to resolve these ambiguities using morphological and geographic data but very few studies have been done using genetic analysis

Field collected specimens representing the currently recognized species were gathered from throughout the southeastern United States and fresh tissue was preserved in silica gel. DNA was extracted from the fresh tissue samples and select recent herbarium specimens via Omega bio-tek E.Z.N.A. HP Plant DNA Mini kit for analysis. Genotypic sequencing was done based on DArTseq technology on the Next Generation Sequencing (NGS) platforms and single nucleotide (SNP) analysis was performed.

This study produces the first phylogeny of the southeastern species of *Amsonia* using unlinked nuclear loci. An assessment of genetic diversity using principal coordinates analysis (PCoA) with single nucleotide polymorphism (SNP) loci as attributes was performed in dartR. We calculated effective population size (N_e), fixation index (FST), and heterozygosity (H_e) using R statistical software. Coalescent simulation and ancestry matrix investigation of species limits, introgression, and hybridization were also performed using the R computer package.

150 - Adapting Tissue Culture Based Authentic Research to the Undergraduate Classroom

Lori Hensley, Kaylee Rawlins, Caitlyn Yongue

Jacksonville State University, Jacksonville, AL

The Cell Biology Education Consortium (CBEC) is an NSF-funded network of faculty and students working to incorporate tissue culture-based research into the undergraduate classroom. While isolated groups are introducing cell culture techniques into such experiences, until now, there has been no coordinated effort to compile resources and provide training that makes creating customizable research projects easier to implement at smaller, primarily undergraduate institutions and community colleges. CBEC members are developing Cell Blocks—technique specific modules consisting of written and video protocols, classroom implementation strategies and assessments. Because all Cell Blocks will have similar basic components, faculty will be able to mix and match multiple blocks to address novel research questions in semester-long course-embedded research experiences (CUREs). All network-created protocols and videos are freely available through the network's website, www.cellbioed.com. This presentation will explain how the Cell Block system works and has been used to develop and implement unique student-driven research experiences. Further, we will discuss how schools can receive technical and financial support through our voucher system and subsidized workshops as well as ways to work creatively with upper administration to receive necessary support. This session is designed for both the beginner, "I do not have a hood," to the seasoned expert.

151 - A CURE for investigating inflammatory response in lung epithelial cells.

Sumali Pandey

Minnesota State University Moorhead, Moorhead, MN

CURE (Course-based Undergraduate Research Experience), is an evidence-based approach to integrate authentic research experience in the curriculum for undergraduate students. Educational scholarship has demonstrated numerous benefits for integrating CUREs into pedagogy; to promote student retention in STEM, foster critical thinking, data interpretation and scientific communication. With this experience, undergraduate students are more likely to pursue research focused careers. CUREs also help faculty to integrate meaningful research into a classroom setting where several students can participate in a research experience at once, and this approach is likely to be time efficient, especially for faculty with heavy teaching loads. At Minnesota State University Moorhead, we are developing a CURE to assess the immune related effects of environmental toxins or immunomodulatory agents. The ultimate scientific goal of this CURE is to ascertain the environmental cues associated with pulmonary inflammation and remodeling, and molecular targets associated with the pathogenesis. The educational goal of this cell block is to involve students in a classroom-based research experience. As a result, stu-

dents learn to mine through the scientific literature, design a research question, hypothesis and an experiment to address their questions. Students acquire skills related to cell culture, cell viability assays and assays for lung inflammation associated biomarkers. Students will be provided with various professional development opportunities to share their findings with the community of scientists. In collaboration with Cell Biology Education Consortium, we plan to share written and video protocols, classroom implementation strategies and assessments with the community of educators.

152 - Incorporating Sustainability in Cell Biology Lab-based Courses

Lyndsay V. Rhodes

Florida Gulf Coast University, Fort Myers, FL

Many scientists would consider themselves eco-conscious and strive to do what they can to conserve the environment, but the impact of scientific research, particularly lab-based research, on the world is often overlooked. It is estimated that general laboratory spaces consume three to five times more energy than comparable office space due to the large energy requirements of commonly used equipment. Additionally, life science laboratories consume high volumes of single-use plastics and generate large amounts of biohazardous waste that requires specialized treatment and disposal. Bench research is costly but clearly invaluable. Our goal is to identify and take steps to decrease the impact of lab-based research on the environment. Cell Biology is a required course for Biology majors at Florida Gulf Coast University that teaches students key techniques in human cell culture. The Lab Sustainability Project engages students in a lab audit to determine the overall environmental cost of the lab practices by measuring energy consumption and consumables. Alternative, more environmentally friendly strategies are identified, implemented, and tested to ensure new methods meet quality standards for research. While there may always be an environmental cost to lab-based science, raising awareness and educating future generations of scientists while implementing intentional strategies can make a significant difference in lessoning that impact.

153 - Changing Mindsets Using Plant Cell Culture and On-Campus Gardens at a Community College.

Gary Bates

NorthWest Arkansas Community College, Bentonville, AR

At NorthWest Arkansas Community College (NWACC) efforts were made to enhance plant courses including Plant Biology and Horticulture. To that end, a CURE sponsored by the Cell Biology Education Consortium (CBEC) was implemented in Plant Biology. Plant Biology is a core science course at NWACC that includes majors and non-majors. This CURE involved plant tissue culture research as part of the course curriculum. To enhance the Horticulture courses, a sustainability garden was established and cared for by students in the Horticulture program. The plants selected for the sustainability garden were of historical importance or rare genotypes intended for conservation. Plant Biology students had the opportunity to propagate some of these heirloom crops in tissue culture and observe the plant's life cycle. Introducing these opportunities into Plant Biology increased student interest in the subject matter and provided context for learning. Students were most interested in tissue culture when observing an importance for cloning these particular specimens based on the plant's rarity and history. The linkage between biotechnology and conservation increased student interest, attendance, and molecular knowledge. Student desire to take further classes in the botanical/horticultural series also increased.

154 - qRT-PCR in Course-Based Undergraduate Research: Creation of a CBEC Cell Block

Amanda Simons

Framingham State University, Framingham, MA

The Cell Biology Education Consortium (CBEC) works to integrate cell culture-based research into the undergraduate classroom. Individual cell blocks are designed to introduce students to specific research techniques and typically include written protocols, a video protocol, and assessment tools. Cell blocks can then be mixed and matched as students build their own projects within the context of course-based undergraduate research. We have developed a cell block for quantitative RT-PCR. Measuring changes in gene expression via qRT-PCR is a cost-effective way for a large number of students to take ownership of an individual research question within a larger project. Validated primer sets for SYBR-green based qRT-PCR are readily available and inexpensive, so individual students or groups can choose their own gene and still share a class-wide protocol and reagents. Results will be shared from students' work measuring changes in gene expression in K562 cells following treatment with resveratrol, completed as part of a senior capstone research course.

155 - CURE Assessment: Impacts and Outcomes from the Cell Biology Education Consortium

Jaime Sabel

University of Memphis, Memphis, TN

This presentation will focus on assessment of Course-based Undergraduate Research Experiences (CUREs) using the Cell Biology Education Consortium (CBEC) as an example. The CBEC is a network of faculty and students incorporating cell culture-based research into the classroom. Project coordinators have collected information on the experiences of both faculty and students, the impact of the research on students, and how the research and educational materials are disseminated. In this session, I will present results from analyses that have assessed the impact of the project and the outcomes for students and faculty. These results will be of interest to anyone involved or interested in developing assessment for CUREs, becoming involved in the CBEC , or building assessment into the development of similar types of networks.

156 - From the Classroom to the Lab: The Role of Exosomes in Regulating Cell Differentiation and Neuronal Repair

Nathan Reyna

Ouachita Baptist Univeristy, Arkadelphia, AR

My lab is a member of the Extra-Cellular Matrix (ECM) division of the Center for Advanced Surface Engineering (CASE). The ECM team is investigating mechanisms for neuronal differentiation and repair. Unlike other cells in our body, when neurons are damaged, they cannot be replaced, and the result is loss of feeling or in some cases, paralysis. By taking a multi-disciplinary and collaborative approach that uses bioinformatics to drive wet lab experiments, we have shown how cells use exosomes to modify their microenvironment. Exosomes are small extracellular membrane-bound vesicles that have a role in cell-to-cell communication. My undergraduate lab has completed four RNA sequencing projects, each showing exosome specific changes in gene expression and cell morphology. Research has now expanded into cell culture experiments. Our results show that exosomes isolated from differentiating neurites (neuron-like) can cause cell differentiation in the absence of neural growth regulators. Research in my lab begins as a Course Embedded Undergraduate Research Experience (CURE) that is then developed into independent student projects. The ECM-exosome project (NSF-AR-EPSCoR) and an AR-INBRE funded project (Lori Hensley-CoPI), was the foundation for the Cell Biology Education Consortium (CBEC – www.cellbioed.com). The CBEC is an NSF funded undergraduate research collaborative network focusing on incorporating cell tissue culture into the classroom. Created in August of 2018, the CBEC now represents over 100 undergraduate institutions and has funded ~ $60,000 in student projects at ten institutions. I will present my lab's data and how collaboration has changed how I approach both education and research. This presentation will be followed by faculty and student discussions on opportunities for others to participate in CBEC activities.

ASB Poster Presentation Abstracts

PP1 - Culturing cells to determine the most economical serum option for a classroom laboratory.

Jenai Dacosta, Josue Fuentes, Elisabeth Javazon, Shoshana Katzman

Georgia Gwinnett College, Lawrenceville, GA

Supplementation of *in vitro* cell cultures with Fetal Bovine Serum (FBS) is customary in most cell culture applications. Currently in the Cell Biology laboratory at Georgia Gwinnett College (GGC), students analyze the growth of mammalian PTK2 (*Potorous tridactylus* epithelial kidney cells) cells in response to a chosen experimental factor over the course of the semester. To decrease the cost of generating cell culture media for this semester long research project, we explored various FBS alternatives that were less expensive than what is currently used. We compared the growth of PTK2 cells supplemented with the current FBS to those supplemented with the FBS alternatives. Once we discover a less expensive FBS that supports cell growth, we will continued efforts to decrease the cost by testing different concentrations of FBS in the cell culture media. Our results will allow GGC, as well as other colleges and universities, to acquire more economical alternatives of FBS to be used in undergraduate teaching laboratories.

PP2 - Adopt a Gene: A Crowd Sourcing Approach to Teaching Computational Bioinformatic to Undergraduates at Regional Universities.

Benjie G. Blair[1], Cynthia Stenger[2], Jeremy Prokop[3]

[1]Jacksonville State University, Jacksonville, AL, [2]University of North Alabama, Florence, AL, [3]Michigan State University, East Lansing, MI

The sciences have seen increasing interest in teaching genomics and bioinformatics to students at the undergraduate and even high school level, [1,2,3,4], and further, to *use these students* to carry out computational bioinformatics and genomics research[4]. The overwhelming volume of available genomic data increases continually and is widely accessible. Improvements in user interface in bioinformatics tools, have served to increase student projects. While it is an attractive solution to consider pulling students into the computational research workforce, there are important issues to consider. The students require training and faculty must limit the number of student researchers they take on. Faculty at smaller universities, with a 4/4 load, may not have much available time or resources for undergraduate research. This project will begin to explore the impact of an undergraduate computational bioinformatics and genomics research experience for students at two regional universities in the South. Both schools "adopted" the same gene, SLC6A1. This gene encodes one of the major GABA transporters, the GAT-1 protein. Mutations in SLC6A1 are associated with seizures, autism and/or epilepsy. Students from both programs followed a common protocol from the Prokop Lab at MSU to analyze data on multiple variants. This includes a sequence-to-structure-to-function workflow [7] comparing their mutation to all gnomAD, TopMed, and ClinVar missense variants for *SLC6A1*. This study contributes to both content development and impact on views about STEM careers. This research opportunity is part of a larger CODE project led by Hudson Alpha Institute for Biotechnology and Educational Outreach at the Prokop Lab at Michigan State University, whose goal is to provide productive, quality research opportunities for community colleges and smaller regional universities, where resources for research are scarce, by providing access to scientists, tools and protocol. [5,6]

PP3 - Development of a no-cost textbook for Cell Biology courses to facilitate student success.

Rebecca Higgins, Shoshana Katzman, Jennifer Hurst-Kennedy, Alessandra Barrera, Jennell Talley

Georgia Gwinnett College, Lawrenceville, GA

Georgia Gwinnett College (GGC) is located in the most ethnically diverse county in Georgia and strives to provide educational opportunities to our student population at an affordable cost. Part of the mission of GGC is to meet the needs of the local population by providing enhanced learning experiences at a low cost. To help meet the mission of the school and the financial needs of its students, providing low-to-no cost textbook options is as integral as providing low cost tuition. We aim to reduce the cost of educational materials needed by a large number of STEM majors attending GGC by providing a no-cost textbook for Cell Biology (BIOL 3400K) a sophomore level course that is a required pre-requisite course for a variety of STEM tracks within the School of Science and Technology (SST). Students that cannot purchase the standard textbook for financial reasons are at a severe disadvantage and will likely struggle to keep up with throughout the semester, resulting in poor academic performance. The Cell Biology Faculty at GGC have spent several semesters identifying 20 specific learning outcomes that will help students demonstrate a clear knowledge of the fundamental components of cell biology. Generation of a no-cost textbook with content directly related to the learning outcomes for the course provide students with a valuable resource that focuses on the content they are required to learn. The development of text, figures and videos that are specific to the expected learning gains will allow instructors to focus on this material and be able to provide additional learning activities and other active learning strategies to promote student knowledge and understanding based on their individual teaching styles.

PP4 - Developing successful ecological research experiences for undergraduates

David Brown, Stephen C. Richter, Kelly Watson

Eastern Kentucky University, Richmond, KY

Most professional scientists first engage in the process of research as undergraduates. Positive early research experiences increase the likelihood of students developing a career as a scientist, and establish a foundation of conduct and skills that will influence their careers. Thus, students, faculty, and administrators should consider how to maximize the benefit of early-career research. We describe a range of types of research experiences for undergraduates, from shadowing to guided-independent research, and discuss key components and fair expectations of undergraduate research experiences for both students and faculty. For students, the benefits of participating in

undergraduate research are often clear: they gain hard and soft skills, knowledge, professional development, and of course, a line on their resume. However, students often do not anticipate the challenges of a successful research experience, including the time requirements and the difficulty of mastering complex scientific skills. We provide suggestions for students to help them create a structured approach to research with specific guidance on developing scientific and people skills, including how to grow relationships with mentors. On the other hand, faculty may be more likely to see challenges, such as perceived loss of time for personal scholarship. The benefits for faculty include the obvious personal satisfaction derived from good mentoring, and if handled correctly, undergraduate research can lead to authentic advances in scholarship. Other benefits for faculty will vary based on the individual and on institutional incentives, such as reassigned time or funding. For faculty, we suggest mentoring best practices, alternative funding mechanisms, and other effective methods of facilitating undergraduate research. Successful undergraduate research also depends on strong support from university administrators, yet those administrators often need to be convinced that limited resources should be committed to non-classroom activities, especially when students come from different institutions. Both faculty and students can help make this case.

PP5 - Teaching Introductory Biology Students to Code

Kevin Drace

Birmingham-Southern College, Birmingham, AL

An increasing part of current biological research requires scientists to use computational methods to analyze incredibly large data sets. Online resources may enable users to analyze, manipulate, and compare data, but an understanding of the computer programming underneath the software is seldom taught outside of specialized courses. As part of a semester-long, course based undergraduate research experience (CURE), we developed an activity for students to manipulate and analyze 16s rDNA sequences using the Python programming language. Students learn the very basics of programming syntax before they edit and analyze their own data acquired throughout the semester. Prior to this laboratory activity, students isolate bacteria, amplify 16s rDNA for each strain using PCR, and purify samples for Sanger sequencing. Each student learns to interpret their chromatogram file before editing each sequence in preparation for BLAST analysis. Approximately, three-fourths of our students come into the course with no programming experience at all, but over one-third have a stated interest in learning how to code. After the activity, the majority of students respond that coding is less complicated than they originally thought and are more confident in their coding abilities. Many of these students also developed an increased interest in coding. Overall, this activity appears to successfully expose students to the power of computational methods in biology and introduced bioinformatics as a viable career path. This activity is accessible to faculty with little to no prior coding experience. Resources to incorporate this activity are freely available to anyone interested.

PP6 - STEM identity - You see me but what do I see?

Loretta Ovueraye

Miami Dade College, Miami, FL

STEM-Mia ("my STEM") focused on success and retention in biology and computer science majors is a National Science Foundation funded project that provides scholarships and supports to academically talented, low-income Science, Technology, Mathematics and Engineering (STEM) students at Miami Dade College (MDC) Padron Campus. Over a five-year period, the NSF - S-STEM funds will support 45 MDC students with scholarships and wrap around services toward preparing them for STEM careers, which are in high-demand and critical to building a competitive workforce that will help grow America's economy. This presentation will discuss the impact on student's STEM self-efficacy and identity of embedding faculty mentoring, discipline immersions, self-analysis, financial support, toward fostering shaping student perceptions of their personal agency at a two-year college. Preliminary results show student self-identify as STEM majors, while having challenges with others perception of them as such. This knowledge will help seeking to incorporate curricular changes focused on success and retention in biology and computer science majors for populations who are underrepresented in STEM fields in general.

PP7 - Integrating science practices with content and core concepts: 3D learning using a unique introductory biology text

Christopher Paradise, Malcolm Campbell

Davidson College, Davidson, NC

Three-dimensional learning is an approach to teaching that integrates science practices (e.g., the core competencies of Vision & Change (V&C)), disciplinary concepts and content, and interdisciplinarity, with cultural and global contexts. Intentional application of 3D learning increases student learning and construction of conceptual knowledge. It can be overwhelming for instructors to redesign introductory biology and choose a textbook aligned with 3D learning and evidence-based practices. Traditional textbooks are inadequate because they have massive amounts of content, yet no integration of global context or science practices. The single dimension of content prevents 3D learning. The National Association of Biology Teachers' Introductory Biology Task Force has adopted 3D learning as it begins to help instructors redesign their introductory biology curricula. One textbook, *Integrating Concepts in Biology* (ICB), by Campbell, Heyer, and Paradise, employs 3D learning and is strongly aligned with the core concepts and competencies of V&C. *ICB* integrates the core concepts of V&C across the biological hierarchy. The core competencies (process of science, quantitative skills, modeling and simulations, and interdisciplinarity of biological subdisciplines) are built into case studies. Ethical, Legal, Social Implications (ELSI) boxes add an extra dimension of interdisciplinarity and cultural context. Bio-Math Explorations (BME) boxes explain how mathematics and modeling are applied to biology. There are more case studies than can be covered in a year-long experience, thus the content can vary depending upon instructor expertise, curricular goals, demographics, and institution type. Many skills are practiced in every case study and quantitative skills are scaffolded across BMEs. Students are asked to apply quantitative skills and reasoning to critically analyze data and construct new knowledge. Multiple examples of how *ICB* employs and scaffolds 3D learning will be shown. *ICB* is presented as a curricular resource for realignment of introductory biology to the 3D learning model.

PP8 - Evaluating and improving undergraduate micropipetting proficiency

John Stanga, Garland Crawford, Kathryn Kloepper

Mercer University, Macon, GA

Our goal is to design, implement, and evaluate best practices for micropipette instruction in undergraduate courses. We have observed large variation in student micropipetting skills in mid- and upper-division biology and chemistry courses despite substantially similar prerequisite coursework. To improve student micropipetting proficiency, we have implemented a set of instructional activities in several biology and chemistry courses, including introductory, intermediate, and upper-division classes. The instructional techniques are designed to improve micropipetting competency by applying peer-interaction, self-reflection, traditional instruction, and targeted interventions. Student outcomes are evaluated by a combination of quantitative and qualitative measures.

PP9 - "Is this bulls**t?" – creating an interdisciplinary learning community to increase information literacy for non-STEM majors

Elizabeth Harrison[1], Thomas Lilly[1], Adrienne Button[2], David Minchew[1]

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Today more than ever, the ability to acquire, evaluate, and use information is essential for our students not only because of the overwhelming amount of information they are exposed to in their classes and in their lives, but also because acquiring and using information is a fundamental part of life in the 21st century. Unfortunately, our students often have limited understanding of what information is and how it is produced and valued, nor do they have the tools and strategies to effectively find and evaluate information and use it to effectively solve problems. Without these literacy knowledge practices and dispositions, our students will not be adequately prepared to meet the demands that are going to remain a central feature of their lives and careers. Learning communities are a high impact pedagogical practice that help students form relationships with other learners, learn how concepts can be applied across disciplines, and enhance student engagement and success. We used the learning community model to improve information literacy skills in our non-major biology students. Professors across three disciplines developed a learning community that was implemented in Fall 2019 for students enrolled in Biological Sciences II (for non-STEM majors), English Composition I, and Introduction to 21st Century Information. The overarching goal of this learning community was to teach our students information literacy by explaining how to detect and deal with bulls**t in scientific and public discourse using Harry G. Frankfurt's text, "On Bulls**t" and Carl Sagan's "Baloney Detection Kit" as course materials. We developed interdisciplinary assignments, communicated regularly about student progress, and evaluated students' communication skills, information literacy, and intercultural awareness. By the end of the semester, students were able to differentiate between different sources of information, research information from various perspectives, and effectively communicate about scientific topics.

PP10 - Scientific Research in the Secondary Classroom: Peer Led Community Learning

Andrea Burzynski, Holly Dunderdale, Megin Rice, Alyssa Weisenstein

Southern Illinois University Carbondale, Carbondale, IL

Traditional science often consists of "cookbook" style labs that include step-by-step instructions with known outcomes. These activities fall short of student involvement in authentic scientific processes. Students' understanding of what they have done or why may be lacking. A transition to authentic labs is needed and holds hope for greater understanding of the content and process of science. These experiences align with science and engineering practices in the Next Generation Science Standards and can help students understand the complexity, uncertainty, and messiness of research. Modern scientific research often requires the collaboration of experts in various fields of study. Therefore, this project was designed to reflect authentic research as a collaborative, interdisciplinary effort of four teachers (chemistry, biology, and pre-calculus) at two high schools. We investigated how students viewed their engagement in authentic research by studying the effect of sunscreens on germination of *Ceratopteris* (*C*-ferns) spores. Chemistry students reviewed the structure of sunscreens, biology students sowed spores and counted germination rates, and math students analyzed the data. All students watched a video on *C*-ferns and their life cycle. Each group of students created a video explaining their portion of the research so that all students understood each stage of the process. Data sources included pre- and post-test surveys, student reflections, and researcher observations. In terms of content knowledge, this approach resulted in improved test scores. Students also demonstrated excitement about doing relevant, authentic research and experienced increased confidence in their abilities to conduct scientific research. There was a high level of student engagement and students concluded with a greater understanding of the nature of science.

PP11 - In Support of Multidimensional Learning: Building a Community of Introductory Biology Instructors through the National Association of Biology Teachers

Kim Sadler[1], Christopher Paradise[2], Anna Hiatt[3]

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Introductory biology is a pivotal course in the undergraduate curriculum for most STEM majors and often the sole science course taken by non-STEM undergraduates. However, multiple entry points and students' diverse backgrounds combined with a broad range of instructor pedagogical and biological training present challenges in providing the ideal introductory biology experience for all students. In addition, there is no consistent assessment of what students know and are able to do after the introductory courses. The National Association of Biology Teachers' (NABT) Introductory Task Force (IBTF) explored these challenges through a survey of nearly 200 introductory biology instructors. Analysis identified out of 2500 examples how many represented integrated core concepts with competencies as recognized in Vision & Change and the AP Bio Framework. Fewer than 5% university, 20% community college, and 50% high school AP instructors utilized a multidimensional approach in their introductory biology course. A multidimensional, skills-based introductory biology curriculum

is not impossible; this shared vision for the introductory biology experience focuses on the intentional integration of key science practice skills or competencies with the desired content focus. This can be accomplished through a multidimensional approach within cultural or global contexts that: 1) includes purposefully scaffolded science practice skills necessary for problem-solving and other 21st Century skills; 2) makes connections with the big ideas across the sciences and other disciplines; and 3) builds content knowledge. The NABT IBTF is developing regional professional development programming for instructors to collaborate within physical and digital spaces to learn and develop curricula for their introductory courses using this curriculum framework. Upcoming opportunities in the southeast include a 1-day regional workshop to be held at Davidson College, Davidson, NC, on Saturday June 13. Additional opportunities to join in the conversation and learn more will be presented.

PP12 - Does active learning have long-term effects? Tracking the persistence and success of at-risk students through the curriculum

Emily Prince, Lisa McDonald

Lander University, Greenwood, SC

In order to address the gap in achievement in biology classes and persistence in the biology program between underrepresented minorities (URM), first-generation college students, low socio-economic status students, and other students, we redesigned Lander University's introductory biology course (BIOL 111) in 2017. The content taught in one semester was divided into two semesters, and the course was restructured to include more formative assessments and focus on active learning. To assess the results of the change, we compared students enrolled in the "old" BIOL 111 from 2015 - 2016 to those enrolled in the "new" BIOL 111 from 2017 – 2018. We assigned students a risk-assessment (RA) score based on their number of risk factors for failure (i.e., URM, first-generation, and low socio-economic status), and tracked students through the program. The change in course structure had a dramatic effect on the success of students in BIOL 111, increasing success rates (i.e., students earning a "C" or higher) from 52% to 70%. The success rate of students with the highest RA score increased from 19% to 51%, indicating a narrowing achievement gap. The percentage of students enrolling in a biology course during the second semester of the freshman year increased dramatically, but the increase did not translate to increased retention in the biology program or Lander University at the sophomore or junior-level. Differences in achievement reappeared in the junior-level Genetics course. While the success rate of students who had taken the old BIOL 111 was only 59%, the success of students who took the new BIOL 111 was 91%, with the most dramatic difference in students with the highest RA scores. We will continue to track students as they progress through the program, focusing on success in upper-level courses and graduation rates.

PP13 - Does course structure matter? Transferring first-year performance gains to upper-level courses

Lisa McDonald, Emily Prince

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In the fall of 2017, we redesigned the biology curriculum at Lander University. Our goals were to increase retention in our program and to increase flexibility within the major. We were particularly interested in addressing the achievement gap between higher risk students (underrepresented minorities (URM), students with low socio-economic status, first-generation college students) and other students. We found that changing the structure of the first biology course in our program from lecture-based to active-learning with increased course structure (more frequent, lower impact assessments) had important, positive outcomes for students with a higher number of risk factors in that introductory course. To investigate whether increased course structure has a similar impact on students in their upper-level courses, we assigned each student a risk-assessment (RA) score (students with more risk factors have a higher score), and we determined whether each upper-level course had a lower-level of structure (at least 70% of course points from exams and quizzes) or a higher-level of structure (<70% of course points from exams and quizzes). We found that students entering the program under the redesigned curriculum had significantly higher final exam scores and significantly higher course grades in their upper level courses than students who began the program in the two years prior to this implementation. The largest gains were observed for students with higher RA scores. This increase in performance was largely independent of course structure; student achievement improved in courses with both higher and lower structure. Our findings demonstrate that students are gaining skills necessary for long-term success in our upper-level courses as a result of the new biology curriculum. Not only are students showing improvement in courses similar to the new first-semester course, but also in more memorization-heavy, lecture-based courses across our program.

PP14 - Alcohol Content and Color Association: A look at the learning ability of the butterfly, *Morpho peleides*

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Insects ability to learn allows them to respond to their environment and change their behavior to optimize resource use. Learning ability has especially been seen in pollinating insects that readily learn to associate floral characteristics such as color, shape, and patterns with rewards such as nectar. *Morpho peleides,* a fruit feeding butterfly, is shown to actively seek out fermenting fruits for sugar and ethanol. The learning ability of *M. peleides* was investigated to determine if they could learn to associate a certain alcohol concentration with a specific color. To determine their ability, a mixture of banana, food coloring dye, and alcohol was offered to *M. peleides* over the span of ten days. The study was split into two sets of trials with each trial having a different combination of alcohol and color, and the number of visits to each station was observed. The results from both trials suggest that there was no significant difference when looking at color and alcohol concentration. These results could have been caused by effects of ethanol on learning, variability of temperature and weather, low sample size, innate color preference, or the use of different environmental cues besides vision. However, there was a significant difference in number of visits at certain location. Each station had a varying amount of sunlight and leaf coverage, making one station more appealing than the others. It was also noted that if there was already one *Morpho* feeding at a station, others were likely to feed at that same station.

PP15 - Staining carbohydrate secretions from kinorhynch glandular cell outlets

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Kinorhynchs are marine animals that crawl in the sediment, feeding on detritus. They are part of the meiofauna along with copepods and nematodes. Kinorhynchs have few structures that differentiate the species, as all members of the phylum have 11 segments and external spines. Spine distribution and secretory glandular cell outlet (gco) positions are important, though gcos are not always easy to identify. In the abundant genus *Echinoderes*, two types of gcos are present. Type one glandular cell outlets (gco1) are located singly and also in serial pairs, on the trunk of the organism. These outlets are actually small fields of minute openings, like a sieve plate. Type two glandular cell outlets (gco2) are also located in pairs, but have a single large opening. We examined *Echinoderes bookhouti*, collected from the Gulf of Mexico, with a variety of stains aimed to characterize the mucus secretions and gco positions. The staining protocols were alcian blue (AB) pH 1.0, AB 2.5, periodic acid-Schiff, concanavalin A-rhodamine, and wheat germ agglutinin-rhodamine. Lectin binding revealed the locations of both types of outlets, particularly gco1, along with the nephridopores of the animals. The histochemical stains were most successful with gco2 secretions and demonstrated the presence of acidic mucopolysaccharides.

PP16 - Health and Behavior of *Danaus plexippus* and Occurrence of *Ophryocystis elecktroscirrha* During Fall Migration through Middle Tennessee

Nicole Pope, Darlene Panvini

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Monarch butterflies (*Danaus plexippus*) migrate seasonally across North America, but these patterns may be constrained by both behavior and parasite occurrence. Specifically, the persistence of protozoan parasite *Ophryocystis elecktroscirrha* (OE) can negatively impact an individual's ability to perform a full migration. Migratory culling could curb the spread of OE, as infected individuals are less likely to survive the full migration. Therefore, late migratory individuals should test positive for OE at a proportionally higher rate given the parasite decreases migratory fitness. This proportion is expected to constitute 7-8% of individuals with OE, typical of regional estimates. These factors were assessed in wild *D. plexippus.* Surveys occurred in and near Nashville, Tennessee in two natural area parks and an agricultural center during the fall migration. Behaviors were noted for all observed individuals, including those not caught. OE prevalence was determined by sampling monarch abdomens. Individuals were tagged to prevent re-sampling. Only one specimen with OE was caught. Currently, a gap exists in the literature for OE prevalence on *D. plexippus* in central Tennessee. Additionally, there is little known about monarch behavior during the fall migration. This study aims to determine the local prevalence of OE and contribute to a better understanding of monarch behaviors during the fall migratory event.

PP17 - Parasites of Bluegill, *Lepomis macrochirus*, from Northwest Tennessee

Vincentiu Olteanu[1], Tom Blanchard[2], Riccardo Fiorillo[3]

[1]Georgia Gwinnett College, GA, [2]University of Tennessee at Martin, Martin, TN, [3]Georgia Gwinnett College, Lawrenceville, GA

We examined the helminth endoparasites of bluegill from a stream in Northwest TN. We'll tell you all about it when we get there.

PP18 - Chemosensory genes and behavior of the terrestrial isopod *Armadillidium vulgare*

Isopods, which belong to the suborder Oniscidea, are one of the few groups of crustaceans possessing aquatic and terrestrial members. Based on paleobiogeographic and phylogentic data, oniscideans most likely evolved fully terrestrial forms for the first time between 100-150 million years ago, much more recently than their extremely diverse arthropod relatives the insects. The common pill bug *Armadillidium vulgare* is one of the most widespread terrestrial crustacean species on Earth, primarily feeding on decaying plant matter. Though previous studies provide evidence of olfactory capabilities, it remains uncertain as to when lineages associated with modern *A. vulgare* first became sensitive to airborne chemical cues. Here we establish the first antennae of *A. vulgare* as a chemosensory appendage in adults by demonstrating its necessity for olfactory-mediated behaviors. We have uncovered highly expressing antennal-specific transcripts in males and females through *de novo* RNA-seq analyses. Genes enriched in the terminal segments of the first antennae of *A. vulgare* represent likely mediators of important olfactory-dependent behaviors like feeding and mating. Annotation of olfactory and other chemosensory genes in this species provides the basis for comparative studies of the independent and perhaps convergent origins of olfaction in *A. vulgare* and other terrestrial arthropods like insects.

PP19 - Characterizing filopodial extensions from hemocytes in the American lobster: effect of a bacterial challenge

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The vascular fluid in the American lobster, hemolymph, contains hemocytes that appear to play a vital role in both immune function and the hemolymph clotting process. Hemocytes interact with each other by first extending filopodia and eventually forming aggregates of a few to several cells. Following an acute bacterial challenge, hemocyte aggregates appear to surround the bacteria, removing them from the hemolymph, in a process we call bacteria clearance. The filopodial extensions from hemocytes appear to be important in the hemocyte aggregation process and by extension, bacterial clearance. We want to know how the presence of bacteria and interference with clotting may affect hemocyte filopodial extension. Four protocols were used: saline only, saline with Glycine Methyl Ester (GME), saline with bacteria, and saline with both GME and bacteria. Hemolymph was drawn into each treatment solution and a small volume of each treatment solution was observed with fluorescence microscopy. The lengths of the filopodia over time were quantified using specialized

measurement software. Average extension for all filopodia extending from selected hemocytes was determined at 5-minute intervals. The fastest rate of filopodial extension occurred for the bacteria alone treatment. The presence of bacteria appears to trigger clotting and suggests that clotting may be important in immune function.

PP20 - Interactions of temperature, *Wolbachia*, and mitochondria in brown widow spiders

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The brown widow spider, *Latrodectus geometricus*, was originally introduced into south Florida, but over the last 20 years, a northern range expansion has been documented. This spider often carries the maternally transmitted bacterial endosymbiont, *Wolbachia pipientis*. While *Wolbachia* can have significant reproductive or fitness effects on its host, the consequences for brown widows are unknown. Introduced populations of brown widows show latitudinal gradient in *Wolbachia* infection frequency, with northern populations having a lower frequency than southern populations. This pattern led us to hypothesize that temperature might be affecting the host-*Wolbachia* interaction. We predicted infected eggs reared in lower temperatures would have either an increased mortality rate or a decreased *Wolbachia* titer than those incubated in higher temperatures. To test this, egg sacs of *Wolbachia* infected (n=4) and uninfected (n=4) spiders were split in half. Half of the embryos from each egg sac were reared in a low temperature treatment and half were reared in a high temperature treatment. The number of unhatched eggs was recorded, and a subsample of offspring were collected on the day of hatching and on the day of first molt. DNA was extracted from each offspring, and quantitative PCR (qPCR) was performed to quantify the relative amount of *Wolbachia* in each individual. No significant difference in mortality rate between temperature treatments was detected, but there was significant decrease in *Wolbachia* density in the low temperature treatment. Because *Wolbachia* and mitochondria are transmitted by the same cellular components during cell division, we hypothesized that the presence of the *Wolbachia* can influence the number of mitochondria. We performed qPCR to quantify mitochondria in the same individuals used in the temperature treatment. A significant positive correlation between mitochondria and *Wolbachia* densities was observed. This result supports hypotheses that mitochondria and *Wolbachia* have evolved a cooperative relationship in cell division.

PP21 - Soil pH as an Indicator of Arthropod Biodiversity and Abundance at an Urban Site in Nashville, Tennessee

Mernaa Fayik, Darlene Panvini

Belmont University, Nashville, TN

The effect of soil pH on vegetation has implications for survival and adaptation of soil dwelling animals, including arthropods. An analysis of biodiversity and abundance of arthropods along a soil pH gradient can provide evidence of how different soil environments might be conducive to supporting certain arthropod life and contribute to variances. The composition of soil arthropod diversity and abundance was compared along a pH gradient at the Belle Forest Cave Property in Nashville, Tennessee using pitfall traps to test the hypothesis that arthropod biodiversity and abundance varies by soil pH. Thirty-six pitfall traps were established in nine quadrats along the pH gradient. Arthropods were sampled once during the fall of 2019. Soil pH and plant diversity were also determined along the gradient. Results comparing the occurrences of arthropods at each site are statistically significant, indicating variation between each site. The bottom plot (least acidic) had the highest family diversity, highest abundance of arthropods, and highest equability. Most similarity amongst families occurred between the top (most acidic) and middle sites on the hill. A comparison with former research exploring the effects of exotic plant species on occurrences of arthropods indicated that soil pH was a stronger determinant of arthropod diversity and abundance than the presence of exotic plants. Results provide baseline data for arthropod abundance and diversity at a protected urban site.

PP22 - The Effect of Gluten on the Epidermis and Lifespan of *Lumbricus terrestris*

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Gluten is a group of proteins found in bread wheat and has been strongly implicated in the development of celiac disease. Celiac disease results from inflammation of the simple columnar epithelium lining the small intestine. The epidermis of earthworms, *Lumbricus terrestris* is also composed of simple columnar epithelial cells. The purpose of this study was to examine the effects of gluten protein on the epidermis and lifespan of *Lumbricus terrestris*. Groups of earthworms were placed into cups of soil containing varying amounts of gluten, gluten-free oat fiber, and regular soil. The results of the study showed that the worms exposed to gluten developed blisters and protrusions on their epidermis and died prematurely, in comparison to worms exposed to oat fiber or plain soil, which remained alive for the entire duration of the experiment and did not develop blisters or protrusions. However, there was no significant difference between the worms exposed to oat powder and the worms in the control group. Therefore, gluten not only has a detrimental effect on the human intestinal epithelium, but on other simple columnar epithelia, such as the epidermis of annelids, as well.

PP23 - Experimental Evaluation of Brown Anoles (*Anolis sagrei*) as Intermediate Hosts for the Invasive Pentastome Parasite *Raillietiella orientalis*

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An Asian parasite (*R. orientalis*) has been found in several species of snakes native to Florida. Snakes become infected with *R. orientalis* when they eat infected prey, but these intermediate hosts are currently unknown. Understanding which species can act as intermediate hosts of *R. orientalis* will enable biologists to determine which species of snakes are likely to be negatively impacted based on their diet

and to predict the parasite's potential dispersal. We fed pentastome eggs, harvested from infected pygmy rattlesnake feces, to 10 brown anoles. We compared them to 10 unexposed control anoles to determine if the lizards could be infected with *R. orientalis* and if infection affected lizard fitness components. The lizards were weighed at capture and again when euthanized. We euthanized both pentastome-exposed and unexposed anoles at several intervals ranging from 5-168 days post treatment. The lizards were dissected using a stereomicroscope and the number and location of parasites were recorded. *Anolis sagrei* did serve as a competent intermediate host, with 70% of exposed anoles hosting multiple pentastome nymphs. The pentastomes were found in the body cavity associated with the surface of the gut, liver, and heart, and in late infections in retroperitoneal areas. The pentastome treatment did not significantly impact survival or growth rate. *Raillietiella orientalis'* use of *A. sagrei*, an abundant and easily transported species, as an intermediate host might facilitate its further rapid geographic spread. This study is the first documentation of any potential intermediate host for *R. orientalis* in North America.

PP24 - Native Antlion Diet: Gaining Weight With Invasive Ants

Kristin Bailey, Jennifer Zettler

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Antlions (Neuroptera: Myrmeleontidae) are insects that are predaceous as larvae. Many species of antlions construct pits in sandy soils that trap ants or other insects. What an antlion consumes as a larva must sustain it through the non-feeding pupal and adult stages. The purpose of our experiment is to determine if there is a difference in the rate of growth and survival of antlions that consume native pyramid ants (*Dorymyrmex bureni*) or the invasive red imported fire ants (*Solenopsis invicta*). Both of these ant species are common inhabitants of open, sandy habitats where antlions construct their pits. Between May and June 2019, we collected 143 antlion larvae (*Myrmeleon* spp.) from a residential location in Savannah, Georgia. The larvae were placed in 2 oz plastic portion cups filled with sifted sand and kept at 25°C. Larvae were randomly separated into 3 treatment groups which consisted of a diet exclusively of either red imported fire ants or native pyramid ants. The third treatment group received an combination diet of the two ant species. Antlions were fed daily totaling 6 ants each week until pupation occurred. To simulate natural conditions, antlions were sprayed with water at least once weekly. Every month the larvae were weighed and their head-capsule widths were recorded to monitor rate of growth. Diet had no significant effect on antlion mortality or head capsule width. However, antlions fed only red imported fire ants showed significantly faster growth and greater weight gains. Our results suggest that in areas where red imported fire ants and antlions overlap, *Myrmeleon* spp. may benefit.

PP25 - You are what you eat: Recycling wastes by rearing larvae that can be used as fish food

Nhien Le, Hannah Grimes, Monisha Prema, Jennifer Zettler, Anthony Siccardi, Brigette Brinton

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Aquaponics is an integrative technology where fish and cultivated plants can be grown together in soilless environments. At Georgia Southern University, the Sustainable Aquaponics Research Center raises tilapia fish in tanks connected to runways with floating vegetable gardens that are enriched by fish wastes. The only organic input in this system is fish food pellets. Produce that is unmarketable can be composted. In a separate facility, GSU has also been operating an experimental 12 lane algal turf scrubber (ATS)™. Used to remediate eutrophic waterways, pumped water is channeled through ATS raceways where algal communities grow and uptake nutrients before the water is returned. While this system is an effective way to remove excessive nutrients, when algae are harvested each week, the biomass itself can become a waste product with a high (~ 30 ppt) salinity. Most waste-products from ATS systems are being sent to landfills. Our goal was to utilize both the waste products from aquaponics and the ATS system and determine if they are suitable as a diet for the larvae of black soldier flies (*Hermetia illucens*). These larvae can then be used as a supplemental food source for tilapia. We reared *H. illucens* larvae on varied diets that included fish solids, algae with different salinities, and decomposing basil and lettuce plants. Our results showed that larvae have higher biomass when reared on a diet containing fresh algae regardless of salinity. Considering that algae are the source for the healthy fats found in the fish, our results suggest that utilizing black soldier flies is a cost-effective way to provide a nutritious food product and while also reducing waste.

PP26 - What happens in forests when nobody's present? A sustainable method to document insect behaviors and interactions using video surveillance

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The federally endangered Schaus' swallowtail butterfly (Heraclides aristodemus ponceanus) inhabits protected subtropical dry forests on several islands in the northern Florida Keys. The larval and pupal stages are particularly vulnerable to native and nonnative predators; however, few published research and reports have identified and quantified predator impacts. Video documentation presents an opportunity to corroborate anecdotal observations (predation events) with empirical evidence. Even in remote areas where electricity is not available, a video surveillance system powered with renewable energy can be used where monitoring wildlife would otherwise be difficult. We documented wildlife activity after captive-bred Schaus' swallowtail caterpillars were released in the field (Key Largo, USA). Video footage revealed two cardinals (Cardinalis cardinalis) captured three Schaus' swallowtail caterpillars within the first 8 h of release. Two caterpillars survived and were active at night. Five butterflies were identified flying onscreen, including the imperiled Florida white (Appias drusilla). A solar powered video surveillance system step-by-step guide with a material list and cost is presented in this paper. The materials and methods can be modified to suit researchers' needs. The video surveillance system can identify culprit species and quantify encounter rates between prey and predators remotely.

PP27 - Assessing insect assemblages at natural and constructed ridge-top wetlands in the Cumberland Ranger District of the Daniel Boone National Forest, KY

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Wetlands support high biodiversity and providing numerous ecosystem services to an expanded landscape, including habitat and source of forage for many organisms. In the Cumberland Ranger District of the Daniel Boone National Forest in Kentucky, more than 400 upland-embedded wetlands (UEWs) have been constructed to provide a permanent water source for bats and other game species. These constructed UEWs are not ephemeral and do not function hydrologically or ecologically as natural wetlands. Bat activity is currently being quantified at sites in the DBNF to compare natural and constructed wetlands. In order to better understand the importance of these wetlands in the context of foraging requirements for bats, we assessed insect activity at 2 natural and 2 constructed UEWs in the Cumberland Ranger District over the summer of 2019 using malaise and sticky traps. Collected insects were identified to the ordinal level, and abundance, richness, and diversity (H') were calculated in the context of wetland type (both trap types) and distance of traps from wetland (sticky traps only). For malaise traps, Kruskal-Wallis analyses indicated no differences between wetland types for abundance or richness ($P > 0.05$), but natural UEWs were less diverse than constructed UEWs ($P \leq 0.05$). Additionally, less insects were captured with sticky traps at natural UEWs versus constructed UEWs ($P \leq 0.05$). Finally, we did not find any evidence that distance from wetland influenced insect captures on sticky traps ($P > 0.05$). This study is important because it piloted methods to be used in continued research on wetlands in the DBNF and can inform future wetland restoration efforts.

PP28 - Identification of Hepatopancreatic Parasites Afflicting Crayfish and Associated Snails in Local Virginia Streams.

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Knowledge of the presence of infectious trematodes or other parasitic organisms dwelling within freshwater crayfish in central Virginia is limited. Related research within Virginia has focused upon trematode infection in Appalachian stream snails, lung helminths in bobcats, and endoparasites in amphibians. Within North America, human infection with the trematode *Paragonimus kellicotti* have been reported, primarily in Mississippi and Midwestern states. *Paragonimus sp.* use crayfish as a primary intermediate host after being released from snails as cercariae. Within the freshwater ecosystems of Central Virginia, snails and crayfish could be potential intermediary hosts for observing trematode presence.

The purpose of this study is to identify the parasitic organism(s) inhabiting the hepatopancreas of crayfish and associated cercariae within snails collected from urban and rural Virginian stream ecosystems. Parasite cyst presence was quantified and compared in relation to the total length (TL) and blotted wet mass (BWM) of individual crayfish. In addition, snails from the study sites will be collected to assess for cercarial presence to support trematode identification. There are three expected outcomes of this study: 1) that parasites will be found in the hepatopancreas tissue of both the urban and rural stream environments and that the prevalence of cysts will be greater in the urban stream habitat; 2) that hepatopancreas parasite presence will be positively correlated with an increase in crayfish size; and 3) that snails from both stream study sites will contain cercaria with greater prevalence in the urban stream habitat. Preliminary examinations of the crayfish hepatopancreas has shown a positive correlation with regards to cyst prevalence in relation to an increase in crayfish TL/BWM. After the identification and intensity of parasitic organisms in the hepatopancreas and associated snails have been completed, application will be made to the effect of crayfish and snail endoparasites with these two distinct Virginia streams.

PP29 - The Effects of Tetracycline on the Reproduction of Rotifers

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Erskine College, Due West, SC

Tetracycline is a commonly used antibiotic in agricultural settings. The runoff of tetracycline disturbs the natural environment of aquatic organisms. The effects of different concentrations of tetracycline on rotifer egg production was examined at for this experiment. Rotifers are microscopic organisms that comprise the lowest level of the food chain. Researching the effects of tetracycline on rotifers is important because the lowest level of the food chain will affect the rest of the food chain depending on their population birth rate. The results of this experiment showed a decrease in egg production when tetracycline concentration was increase.

PP30 - New state record and range extension for Fitch's Elephanthopper (*Fitchiella robertsoni* (Fitch))

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Fitchiella robertsoni (Fitch's Elephanthopper) is a small planthopper in the family Caliscelidae that is characterized by a bulbous process covering much of the face. It was previously known in a few grassland types in 11 US states and is considered extremely rare wherever found. This new state record, discovered in Sumter County, AL, extends the range of this planthopper and accounts for the 21st known population.

PP31 - Characterization of chemical senses in a terrestrial isopod

Tate Powell, Jackson Sparks

High Point University, High Point, NC

Isopods, which belong to the suborder Oniscidea, are one of the few groups of crustaceans possessing aquatic and terrestrial members. Paleobiogeographic and phylogenetic data suggest oniscideans likely evolved fully terrestrial forms for the first time between 100-150 million years ago, much more recently than their extremely diverse arthropod relatives the insects. The common pill bug *Armadillidium vulgare* is one of the most widespread terrestrial crustacean species on Earth, primarily feeding on decaying plant matter. Though previous studies provide evidence of limited olfactory capabilities, chemosensation has not been comprehensively examined in isopods. Here we establish the first antennae of *A. vulgare* as a chemosensory appendage in adults by demonstrating its necessity for avoidance of plant-derived repellents at a short distance. We have uncovered highly expressing antennal-specific transcripts in males and females through *de novo* RNA-seq analyses. Genes enriched in the terminal segments of the first antennae of *A. vulgare* represent likely mediators of important behaviors like feeding and mating. Annotation of olfactory and other chemosensory genes in this species provides the basis for investigating the independent and perhaps convergent origins of olfaction in *A. vulgare* as compared to other terrestrial arthropods like insects.

PP32 - Molecular identification of a novel *Limnodrilus* worm (Annelida, Clitellata, Naididae, Tubificinae) found in at Blount Springs, Blount County, AL

Mariel McConville, David A. Johnson

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Blount Springs, a sulfur springs in Blount County, AL, appears to be a site with a diverse micro- and macrobiota based on our earlier studies. We discovered an annelid of genus *Limnodrilus* at Blount Springs in 2017. In this study, we used DNA sequence analysis of nuclear and mitochondrial segments to clarify the identity of this worm. Based on our phylogenetic analyses, this worm appears to be most closely related to the species *Limnodrilus hoffmeisteri III*, which is a member of the *L. hoffmeisteri* species group. Before our discovery, *L. hoffmeisteri III* was only known from two sites: one in Illinois, USA, and one in Belgium, both normal, fresh-water sites. Interestingly, the Illinois worm and the Belgian worm appear to be more closely related to each other than to our worm. Our worm then appears to be both a geographical extension of its range as well as a habitat extension.

PP33 - Prevalence of *Wolbachia* in Local Populations of Cockroaches in the Southeastern US

Brian Kohler

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Wolbachia is a bacterium that infects the reproductive organs of approximately 20% of insect specimens. Yet, preliminary surveys of cockroach populations in coastal Georgia show that approximately 40% test positive for *Wolbachia*. This bacterium is known to affect the host's physiology in four distinct ways: parthenogenesis, cytoplasmic incompatibility, male-killing, and feminization. The purpose of this study is to determine if the prevalence of infection in cockroaches varies by species and/or by their locations. This project involves a large-scale survey of cockroach species in Chatham County and the surrounding areas to more effectively determine the rate of *Wolbachia* infection in regional populations. Cockroach specimens were collected, stored in vials filled with 70-80% alcohol and kept frozen at -20°C. Then, used the combined procedures of DNA extraction, PCR, and gel electrophoresis to determine infection rate. To date, over 250 individuals from 14 species of 3 families have been collected from 21 locations. Future studies should investigate why the prevalence of *Wolbachia* is atypically high in species in the family Ectobiidae as well as ascertain the potential phenotypic effects it might have on members of that family. Understanding prevalence and the symbiotic role of *Wolbachia* in cockroaches can help determine population control mechanisms for these peri-domestic insect pests.

PP34 - Prevalence of *Borrelia burgdorferi* in Central Florida Rodents

Terykah Hollis, Sean Beckmann

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Lyme disease is the most common tick-borne disease in the United States, yet it is considered uncommon in Florida. While there are relatively few cases each year, little research has focused on identifying reservoirs of the bacterial agent, *Borrelia* burgdorferi, in this region. By comparison, many studies have focused on reservoirs of *B. burgdorferi* in the northeastern, midwestern, and western United States. The few studies that have focused on *B. burgdorferi* in Florida have identified low infection rates in rodents throughout the state with the exception of the extreme northeastern region. However, these studies have focused on relatively few animals, making it difficult to apply their results. Our study sought to identify the prevalence of *B. burgdorferi* in rodent hosts in central Florida. To accomplish this, small mammals were trapped and tissue samples were collected at Lake Woodruff National Wildlife Refuge. Tissue samples were screened for *B. burgdorferi* via nested PCR of the OspB locus and results were verified by DNA sequencing. Of the four rodent species sampled, two showed evidence of infection with *B. burgdorferi sensu stricto*. There was a 29.4% infection rate in *Peromyscus gossypinus* and a 76.9% infection rate in *Neotoma floridana*. Contrary to the findings of other studies, neither *Ochrotomys nuttalli* (n=2) or *Sigmodon hispidus* (n=7) showed evidence of infection. However, sample sizes of both species were insufficient to draw conclusions of their reservoirs status. While additional research is needed, both *P. gossypinus* and *N. floridana* are possible reservoirs of *B. burgdorferi* in central Florida.

PP35 - Identifying *Wolbachia* Strains Found in *Aedes Albopictus* mosquitoes through Multilocus Sequence Typing (MLST)

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Wolbachia is the most common bacterial endosymbiont in arthropods, and is passed from mother to offspring during egg deposition. In insects, *Wolbachia* has evolved reproductive manipulations to increase the proportion of infected females in a population, and one such mechanism, Cytoplasmic Incompatibility (CI), is the most prevalent manipulation in insects. During CI, mating with an infected female results in the production of viable offspring. However, if an uninfected female mates with an infected male, the resulting embryos die during development. Mosquitoes are known to harbor *Wolbachia* and have their reproduction manipulated by CI. We are attempting to determine if local populations of mosquitoes can be controlled utilizing *Wolbachia* and CI and thus reduce the spread of various arboviruses, such as Dengue and Zika. Approximately 35 known strains of *Wolbachia* have been identified, but the identity of local strains have not been confirmed. We are attempting to identify the the specific strains of *Wolbachia* in the local population of *Aedes Albopictus* mosquitoes utilizing Multilocus Sequence Typing (MLST) described by Laura Baldo. Individual *Aedes Albopictus* mosquitoes are known to harbor two specific strains of *Wolbachia,* wA*lb*A and wA*lb*B. Here we report our efforts to confirm the presence of both supergroup A and B strains of *Wolbachia* in the local Savannah population. Previous sequence and DNA analysis of *Wolbachia* specific genes, identified genes found only in wA*lb*B. However, PCR analysis using primers specific for wA*lb*A or wA*lb*B amplified DNA fragments from both strains of *Wolbachia* confirming that local individuals carry both strains *of Wolbachia.*

PP36 - A Test of Differential Predator Avoidance by Blue Ridge Two-Lined Salamanders (*Eurycea wilderae*)

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Predation can be influential in the maintenance of parapatric distributions if the parapatric species respond differentially to potential predators. The Blue Ridge Two-lined Salamander (*Eurycea wilderae*) occurs in Appalachian streams, and *E. cirrigera* occurs in Piedmont streams, swamps, and ponds. The two share a parapatric border along the Appalachian foothills where they are narrowly sympatric. Earlier work demonstrated that larval *E. cirrigera* avoids the lotic, upland fish *Cottus carolinae* but not the lowland, lentic *Lepomis gulosus*. If these predators contribute to parapatry in these salamanders, we predicted that *E. wilderae* would avoid *L. gulosus*. We tested our predictions by replicating the earlier procedure used with *E. cirrigera*. We placed larval salamanders in a water-filled trough with a wire cage at one end. There were three treatment groups: (1) an aerated, fishless cage for a control, (2) an aerated cage with *L. gulosus*, and (3) an aerated cage with *C. carolinae*. Surprisingly, *E. wilderae* did not respond significantly to either predator. Because our *E. wilderae* larvae came from a fishless location, their lack of response may be due to their unfamiliarity with fish as predators. However, it is worth noting that we observed predatory crawfish in close proximity to salamander larvae. Future research using crawfish could determine whether this salamander reacts to predators with which it is familiar. Regardless, the absence of avoidance of a lowland predator suggests that predator avoidance by larvae does not contribute to maintaining the parapatric boundary with *E. cirrigera*.

PP37 - Potential Differential Infection Rates in the cryptic salamanders *Desmognathus folkertsi* and *D. quadramaculatus* by the Trematode *Metagonimoides oregonensis*

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Metagonimoides oregonensis is a little-known, digenetic trematode that uses raccoons as definitive hosts. In the southern Appalachians, it uses stream snails (*Pleurocera*) and salamanders (e.g., *Desmognathus quadramaculatus*) as first and second intermediate hosts, respectively. Although *D. quadramaculatus* often occurs sympatrically with its cryptic congener *D. folkertsi*, other parasites discriminate between these two species. The purpose of our research was to test whether *M. oregonensis* also discriminates between the two. We were unable to find a location with both salamander species and the appropriate snail species. Therefore, we collected larval salamanders from two allopatric sites within the same county where each salamander occurs with the snail: 1) Frady Branch of the Broad River system and 2) Rothwell Creek, a tributary of the Tugaloo River. Both streams are part of the Savannah River drainage in Stephens County, Georgia. Using a dissecting microscope, we counted all visible metacercariae in the trunk of each salamander. As a surrogate measure for salamander size, we measured head width. All *D. quadramaculatus* (N = 23) were infected (mean ± 1 SE = 56.30 ± 10.91; range = 18–173). There was a significant relationship between head size and number of metacercariae (P = 0.022), a probable indication that older larvae accumulate more parasites. None of the *D. folkertsi* (N =23) was infected. Although our data suggest that this parasite is more specific to *D. quadramaculatus* than to *D. folkertsi*, we will need to test incident rates where all of them co-occur before we can be certain.

PP38 - Peaks of Otter Salamander *(Plethodon hubrichti)* Condition: Optimal Elevation for this Montane Species of Salamander

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The Peaks of Otter Salamander (*Plethodon hubrichti;* POS) is a montane species found at elevations above 442 m within a 117 km^2 area of the Blue Ridge Mountains in central Virginia, USA. In allopatric areas (areas without the Eastern Red-backed Salamander, *P. cinereus*, a potential competitor), salamander condition was hypothesized to be optimal at elevations near 1000 m and then decrease below and above this elevation. Decreased condition at lower elevations would most likely be due to increased temperatures and lower humidities, which may adversely affect the ability of salamanders to forage effectively. Decreased condition at elevations above the optimum would

likely be caused by a shortened active season due to the colder temperatures at these elevations. In October 2018, *P. hubrichti* were collected by turning over rocks and logs at eight sites ranging in elevation from 518 to 1143 m. The mass and snout-vent-length (SVL) of females were recorded at each elevation. From the SVL and mass data, residual salamander condition index was calculated, which was then regressed against elevation. Average condition declined from a high of 0.24 at 1128 m to a low of -0.15 and -0.03 at 518 and 1143 m, respectively. This information indicates that the optimal elevation for the POS is around 1128 m. Based on these results, the residual condition index is a simple method for assessing the effects of elevation and can be used as a surrogate measure for density and reproductive output since they follow similar trends across elevations. These results also support the importance of conserving mature hardwood forests, particularly at lower elevations, which represent marginal environments for *P. hubrichti* as evidenced by their low condition index values.

PP39 - Modeling Arboreal Habitat Selection in the Green Salamander (*Aneides aeneus)*

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The Green Salamander (*Aneides aeneus)* is a partially arboreal cliff specialist distributed from southwest Pennsylvania into Alabama and Mississippi along the Appalachian Mountains, with special protected status in several states. Green Salamanders occur in both rock outcrop and arboreal habitat throughout the active season, although little is known about the latter mode of habitat use in this species. We addressed this lack of knowledge through a season-long survey of arboreal habitat use within an abundant Green Salamander population at Flag Rock Recreation Area in Norton, Virginia during 2019. We specifically surveyed 40 randomly-selected trees surrounding rock outcrops for Green Salamanders during weekly visits to this site to determine which arboreal habitats were occupied by the species. In addition, we characterized the following variables that may be drivers of arboreal habitat use: number of available refugia (crevices in bark, hollow limbs), distance to rock outcrop, tree size (diameter at breast height), canopy cover, tree height, and tree species. We additionally recorded microclimatic variables, Julian date, and time of day as survey covariates, using a single-season occupancy modeling approach to analyze arboreal habitat selection in Green Salamanders at this site. Our models indicated that probability of detection was negatively associated with temperature and moisture, likely the result of salamanders moving between rocks and adjacent trees during periods of wet weather. Probability of occupancy was highest in smaller trees, tree surfaces beneath greater canopy cover, and in trees with a small number of suitable refugia. Our model indicates that Green Salamanders non-randomly select arboreal habitat around rock outcrops based on attributes specific to individual trees, emphasizing the importance of maintaining linkages between outcrop and forest habitats as a management practice for conserving Green Salamander populations.

PP40 - A Re-Examination of Body Size Reduction in *Plethodon yonahlossee* Populations due to Climate Change

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Climate change is rapidly altering Earth's natural systems. Some organisms, such as amphibians, are particularly vulnerable to these detrimental effects. One documented response to climate change by some taxa is to reduce body size. Recent research has found evidence for reduction in body sizes of several salamander species from the genus *Plethodon*, including one of the largest species, *Plethodon yonahlossee*. However, the sample size for *P. yonahlossee* was small (n=36) relative to the other *Plethodon* species examined. Therefore, we re-examined the possibility of body size reductions in *P. yonahlossee* populations from North Carolina over time. We measured snout-vent length (SVL) and head morphology of 189 specimens collected from 1979-2004 in North Carolina. We were also able to account for museum shrinkage when data was available. We found evidence for declines in SVL over time. We also found significant differences in head morphology; however, site rather than time was significant. We also found original SVL measurements made at or near the time of preservation was significantly larger than measurements made in 2019, indicating museum shrinkage had taken place. The significant decline in SVL over a 25-year period represents a rapid phenotypic change, adding further evidence to the literature of body size reduction as a strategy of salamanders in response to climate change.

PP41 - A preliminary comparison of Eastern Hellbender (*Cryptobranchus alleganiensis*) habitat across the Ridge and Valley province of southwest Virginia

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The Eastern Hellbender (*Cryptobranchus alleganiensis*) is a secretive amphibian preferring clean, clear, fast-flowing streams across the Appalachian Mountain region. Increasing hellbender declines and associated conservation concern have led to the development of stream restoration initiatives aimed at restoring hellbender habitat in degraded streams. However, little is known about the specific habitat requirements of hellbenders in understudied parts of their range, a factor that inhibits the design of restoration projects. We performed habitat and environmental DNA (eDNA) surveys for hellbenders across 11 watersheds in the Ridge and Valley province of southwest Virginia, with the goal of comparing habitat characteristics (catchment-scale land use, water quality, fine sediment intrusion, substrate size/type, and channel morphology) across sites with and without known hellbender populations. We found no significant difference in habitat structure across streams with and without historic hellbender records. However, we did uncover that streams within this region fall into two general, statistically-distinct habitat types: high-gradient streams characterized by step-pool morphology and larger boulder cover and valley streams characterized by riffle-run-pool-glide morphology and higher amounts of bedrock slab substrate. Hellbenders are known from both stream types in our study region, suggesting that there is not a single, "one size fits all" habitat type preferred by hellbenders across southwest Virginia's Ridge and Valley province. These results indicate that regional conservation programs targeted towards the restoration of hellbender habitat will likely need to account for these higher-order differences in stream structure.

PP42 - Modeling the spatial distribution and habitat association of Plethodon punctatus, the Cow Knob salamander

Jack Doss

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Virginia is a global hotspot for salamander diversity. Many species of which are endemic and have narrow ranges with specific environmental and habitat requirements. This project focuses on the spatial distribution and habitat association of Plethodon punctatus, the Cow Knob salamander. P. punctatus is a rare species and is of conservation concern to the US Forest Service. P. punctatus is considered to be a habitat specialist, occupying higher elevation (>≥3000ft), north facing rocky talus slopes on Shenandoah mountain in western Virginia and eastern West Virginia. This project aims to quantify the association this species has with that talus habitat across a range of environmental conditions, as well as with interactions with sympatric salamander species such as Plethodon cylindraceus, the White Spotted Slimy salamander, and Plethodon virginia, the Shenandoah Mountain salamander. Visual encounter surveys will be used to collect unbiased locations of P. punctatus individuals, as well as individuals of sympatric salamander species. Microclimate data will be collected during surveys. Environmental, climate, and location data will be used to construct a habitat model to predict where P. punctatus may occur in order to assist in conservation efforts for the species.

PP43 - An eDNA survey of the wood frog, Lithobates sylvaticus, in Northern Alabama.

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Wood frogs (Lithobates sylvaticus), are True Frogs of the family Ranidae. Their geographic range extends from above the Arctic Circle to as far south as northern Alabama, including Calhoun, Clay, and Talladega Counties (Mount 1975). Little is known of wood frog biology in Alabama. Wood frogs breed in vernal pools in late winter, then disperse widely from the ponds during the rest of the year. Short breeding seasons and wide dispersal make wood frogs difficult to catch and survey. Additionally, wood frogs are at the southern limit to their distribution in Alabama. Wood frogs lose their ability to right themselves when inverted at roughly 92°F (Bratstrom 1963). If climate change continues to cause increased temperatures, then wood frogs may become extinct in Alabama. In order to establish baseline data on the distribution of wood frogs in Alabama, we propose to use eDNA techniques to survey potential wood frog habitat.

PP44 - Impacts of an invasive honeysuckle, *Lonicera maackii*, on embryonic and larval anurans and their associated invertebrate communities

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Wetlands are particularly vulnerable to invasive plants because seasonal movements of sediments, water, nutrients, and debris from adjacent terrestrial habitats can create ecological conditions suitable for invasions. Amur honeysuckle (*Lonicera maackii*) is an abundant invasive shrub in the eastern United States, but relatively few studies have examined the ecological impacts of its leaf litter in wetland systems. We assessed effects of honeysuckle leaf litter on embryonic hatching success, survival, and growth of Northern Cricket Frog (*Acris crepitans*) larvae, oviposition preference by female Cope's Gray Treefrogs (*Hyla chrysoscelis*) and associated tadpole survival, and both short- (~3 weeks) and long-term (~2 years) effects on aquatic invertebrate communities and abiotic parameters. Honeysuckle leaf litter reduced both hatchling survival and subsequent growth in laboratory experiments. In mesocosm experiments, honeysuckle reduced dissolved oxygen, algal biomass, and macroinvertebrate abundance in short-term mesocosm experiments, while increasing duckweed cover in long-term experiments. Female treefrogs preferentially selected mesocosms without honeysuckle for oviposition, and tadpole survival in mesocosms with honeysuckle was drastically reduced. Short-term effects of honeysuckle leaf input are severe, especially the high mortality rates of *H. chrysoscelis* from starvation or suffocation. The entire food web is altered when the algal food source is removed and the macroinvertebrate communities are changed. This has broader implications for the function of wetlands and the connection between forest and wetland systems through adult amphibian migration. A future study could assess the recovery of the wetland after the leaf litter input, as it appears that effects are strong initially but lessen over time.

PP45 - Morphology of the Eastern Kentucky Copperhead and Recurrence at a Campsite.

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Eastern copperheads (*Agkistrodon contortrix*) are predominantly characterized as sit and wait predators, but have been noted to actively forage for emerging cicadas. This is a distinct change in behavior because sit and wait predation is considered more energetically efficient and the foraging sites are open, exploiting the copperhead's protective coloration. However, because this behavior has been frequently observed, there must be an underlying advantage. This study aimed to identify a possible advantage to active foraging by determining if there was a relationship between the body condition of an individual snake and how often it was recaptured. As part of an ongoing mark recapture study, data were collected at each instance of recapture including PIT tag ID number, snout to vent length, mass, and sex. There was not a direct relationship between body condition and recurrence (the number of instances of recapture). Instead, variation in body condition and recurrence can most likely be attributed to the time females spend gravid or preparing for gravidity. In addition, an increase in range of body conditions over three years was recorded, which may be attributable to weather conditions; this is an interesting potential relationship to explore further. In future studies, a focus will be taken on increasing surveillance and recaptures to procure an accurate daily account of the individuals in the campsite as well as increasing the measurements taken per individuals.

PP46 - Seining for stream salamanders: Season and site matters but not time of day

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Sampling for salamanders in streams can be challenging as different techniques can lead to biased estimates of populations. One type of stream sampling that has been underutilized for assessing salamander abundance is kick-seine sampling. Currently it is unknown if kick seining is a viable method for estimating salamander abundance and salamander body condition. Therefore, we conducted a study to investigate how stream salamander abundance and body condition changed across seasons and during the time of sampling (day versus night) using kick seining. We sampled six streams in western North Carolina every three months over a 12-month period in 2019-2020. Each stream had a 10-m stretch that was sampled during diurnal and nocturnal sessions on the same day. We found that salamander abundance significantly differed by site but not by time of day and season. Salamander body condition varied also by site and season but not time of day. Our study indicates that kick-seine sampling is a viable technique to estimate stream salamander abundance. It also suggests that kick-seining sampling yields similar abundance estimates regardless of the time of day but that seasonal variation does exist. Overall, future work should consider comparisons of kick seining to other stream salamander sampling techniques.

PP47 - Adult breeding phenology potentially informs larval competitive environments of two pond-breeding salamanders

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Phenology, or the timing of life history events, can vary depending on seasonal abiotic variation and site-level differences. In amphibian communities, timing of breeding events and arrival order of species to breeding sites can indirectly influence larval competitive interactions and ultimately, whole pond community structure. To better understand the variability of arrival times and the indirect effect of this variation on larval community composition, we monitored breeding phenology and larval size of two fall-breeding salamander species, the Marbled Salamander (*Ambystoma opacum)* and the Ringed Salamander (*Ambystoma annulatum*) in central Missouri. We used drift fences to partially enclose approximately 50% of three wetlands. Each fence had an entry point with a wildlife trail camera mounted above. Cameras operated in the fall of 2017 and 2018. For larval densities and size, we surveyed the same three wetlands in the spring of 2018 and 2019 following camera deployment; mesh minnow traps were deployed for 2 trap nights, and all captured larvae were photographed. All photographed larvae were measured for snout-vent-length using ImageJ. In 2017, we captured images of 37 *A. opacum* and 139 *A. annulatum* migrating to or from wetlands, while in 2018 we captured images of 63 *A. opacum* and 46 *A. annulatum*. At two sites in fall 2018, more adult *A. opacum* than *A. annulatum* entered each pond. At those same sites in spring 2019, *A. opacum* larvae were smaller than *A. annulatum* larvae, indicating intraspecific competition may have occurred. Additionally, we captured images of 17 other species of herpetofauna and 11 species of non-herpetofauna, suggesting that camera traps may be a useful and non-invasive tool for monitoring amphibian movement and predator presence at wetlands. Our results highlight the seasonal variation in amphibian communities, and the potential importance of competitive interactions within the larval stage.

PP48 - Southeastern Anuran Call Identification Using Attention Based Neural Networks

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Initiatives such as FrogWatch and the North American Amphibian Monitoring Program (NAAMP) organize, recruit, and train volunteers for large scale anuran population monitoring. Without the efforts of these citizen scientists, anuran conservation efforts would be restricted by the availability of qualified field biologists. After qualifying for capacity to identify regional calls, volunteers sample anuran populations by documenting the presence and intensity of calls at select habitats. Automating call identification would reduce both the qualifications necessary to contribute in these projects, and the potential subjectivity associated with determinations made by different researchers. Here we present the results of using an attention based convolutional neural network to automate call identification. The network was trained to differentiate 13 southeastern anuran calls using field recordings available through iDigBio. Attention modules are utilized within this network to retain sequential context when evaluating the diverse and relatively noisy field recordings. Although expanding this method to recognize additional taxa will be necessary for distributed services, we demonstrate the method's potential to expand anuran monitoring in the face of species decline throughout the southeast.

PP49 - Investigating the Distribution and Taxonomic Status of *Eurycea wilderae*.

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Scientists have been investigating the distribution and taxonomic status of *Eurycea bislineata* and have been applying molecular biology techniques since the 1980s. The three traditionally recognized subspecies are *E. b. bislineata*, *E. b. cirrigera*, and *E. b. wilderae*. Recent molecular research suggests that the current taxonomy of two line salamanders under represents the evolutionary diversity. However it is unclear which existing binomials should be applied to which populations of *Eurycea*. Here we focus on the taxonomic and distributional status of *Eurycea wilderae* by comparing topotypic material with populations collected throughout the range of *E. b. cirrigera* and *E. b. wilderae*. Our results suggest that the distribution of *E. b. wilderae* is vastly different from published range maps. Furthermore, our molecular phylogenetic reconstruction and statistical analysis of linear morphological measurements demonstrates unequivocally that most populations currently referred to as *Eurycea wilderae* are in fact other species.

PP50 - Eliminating Bias: A comparison of caliper and image-based techniques for morphometric measurements

David Weisenbeck, David McLeod

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Traditionally studies of morphology have relied on caliper-based measurements of specimens. Because this method results in observer-specific biases that can affect the precision, utility, reproducibility, and confidence in statistical analyses of these measurements, best practice has dictated that all measurements are taken by a single observer. While this reduces some of the issues in a single study, it can limit accurate comparisons between studies. This project tests a method for digitally measuring specimens that reduces observer errors and biases associated with manual caliper-based measurements and provides a means for reliable comparison of data collected by multiple individuals. Morphometric data were collected for 14 morphological characters using both manually operated Vernier calipers and from images of specimens (frogs) using ImageJ software. We test for differences within and between replicate sets of digitally and manually acquired data to determine whether these methods are truly comparable and which results in the greatest precision. We also test the replicability of the digital method by comparing measurement data from multiple observers.

PP51 - Using Anchored Data Set of Seepage Salamander (Desmognathus aeneus)

Henri Vega-Bernal

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Seepage salamanders are amongst the tiniest vertebrates in North America and are one of the smallest species of the genus Desmognathus (less than 60mm in length). With concomitant small home ranges (typically less than 1 m^2), they are distributed across a vast geological region, ranging from the Appalachian Mountains of western North Carolina, southwest into Alabama. Because these factors provide the geographic and evolutionary context for diversification, we wanted to test whether there is strong genetic structure across the range. Seepage salamanders are currently recognized as a single species, however, based on NGS data of 400 loci collected from ~50 localities, suggests there are six distinct clades within Seepage Salamanders.

PP52 - Progesterone Receptor Dynamics: *Effects of Immunomodulation on Receptor Expression in HeLa Cells*

Christopher Brandon, Bagie George

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In these experiments HeLa cells were maintained in culture in MEM + 10% FCS. For experimental trials, HeLa cells were seeded in 96 well plates at a density of 30 x 10^3 cells/well and stimulated with varying concentrations of progesterone. To determine calcium dynamics, a Fluo-4 NW calcium assay kit (Molecular Probes) was utilized. Briefly, 100 ml of the dye loading solution was added to each well and allowed to incubate at 37°C for 30 min followed by room temperature for an additional 30 min. Fluorescence was then measured on a flow cytometer using instrument settings appropriate for excitation at 494 nm and emission at 516 nm. Results indicated a 40% increase in calcium mobilization at all concentrations of progesterone. These results are encouraging for further studies into the mechanisms of calcium dynamics in mammalian cells.

PP53 - Gene upregulation in the acute transcriptome response of the midbrain/diencephalon to injury in the mummichog.

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Unlike mammals, fish produce new cells throughout their central nervous system during the course of their lives and thus, maintain a tremendous capacity to repair damaged neural tissue. Much of the focus on understanding the neural regenerative capacity of fish has been directed at regions of the brainstem, forebrain, and retina; however, the mesencephalon (midbrain) and diencephalon have received little attention. We sought to characterize the whole transcriptome response of the midbrain/diencephalon to injury in the adult fish. Further, we begin examining the temporal profile of genes in the adult fish midbrain/diencephalon reparative process from acute to chronic times of recovery. Using the mummichog (*Fundulus heteroclitus*), we administered a mechanical lesion traversing the midbrain optic tectum, tegmentum and underlying diencephalic hypothalamus and then used RNAseq to examine differential gene expression in response to the lesion at an acute recovery time of 1hr post-injury. Comparisons of whole transcriptomes, derived from isolated RNA of intact and injured midbrain/diencephalic tissue, identified over 400 differentially expressed genes (DEGs) with False Discovery Rates (FDRs) of either $q < 0.1$ (181 genes) or < 0.4 (404 genes). The vast majority of DEGs were putatively upregulated and, based on functional annotation, showed that the injured tissue was engaged in cellular processes such as proliferation and neurogenesis. Using qPCR, we validated the upregulation of three DEGs, *pim-2*, *syndecan-4*, and *cd83*, as well as an example of a non-differentially expressed gene, brain *insulin-like growth factor* (*igf-1*). Though not differentially expressed at 1hr post-lesion, the temporal profile of brain *igf-1* indicated significant downregulation at 48hr post-lesion in injured midbrain/diencephalic tissue relative to non-injured tissue. These data provide an extensive molecular profile of the injury response of a brain regenerative-capable adult vertebrate and insight into the wide-range of cellular processes involved in successful brain repair.

PP54 - Optimization of Culture Conditions for the Simultaneous Recellularization of Porcine Internal Thoracic Artery Scaffolds with Multiple Cell Types

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The increasing prevalence of ischemic diseases has generated a growing need for heart bypass surgeries. Vascular grafts currently used in bypass surgeries have limitations and can fail or become occluded. The ultimate goal of our research program is to tissue engineer vascular grafts from scaffolds derived from decellularized porcine internal thoracic arteries that can be recellularized with patient specific cells and restore function more effectively than current methods. The ability to recellularize scaffolds with multiple cell types, including endothelial cells (EC), smooth muscle cells (SMC), and possibly adipose-derived mesenchymal stem cells (ADSCs) is important for imparting function to an engineered vessel. However, an important question that arises in such work is what type of cell culture media should be used to allow the different cell types to grow together during the scaffold seeding/culture process? We hypothesized that mixtures of two media types that support growth of two of the cell types of interest could be identified. To test our hypothesis, we grew ECs in different combinations of 1) EC and SMC medium and 2) EC and ADSC medium. We also grew ADSCs in different combinations of EC and ADSC medium. We used the alamarBlue assay to monitor the viability of the cells over 72 hours of culture. We used flow cytometry to assess the expression of CD31 on ECs cultured in different media combinations. In all cases, the growth of the cell type of interest was no different in a 50:50 combination of its medium and the other medium than growth in 100% of its own medium. In addition, CD31 expression was maintained in ECs under all experimental conditions tested. These results suggest that the use of 50:50 mixtures of culture medium will support the growth of the cell types of interest following their simultaneous seeding into our vascular scaffolds.

PP55 - Potential Predictors of Nodal Metastasis in Early Tongue Cancer Found Through Aperio Image Analysis

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Introduction: Excessive use of cigarettes cigars/ pipe as well as smokeless tobacco is one of the most common cause of oral cancer. In Shaukat Khanum Memorial Center Hospital and Research Center (SKMCH&RC) in Pakistan, Squamous Cell Carcinoma of Tongue (SCCOT) is the second most common head and neck malignancy. Approximately 20-30% of patients with early oral tongue carcinoma will have occult neck nodal modal metastasis. Presently, elective neck dissection remains the only reliable way to predict regional and or distant metastasis. There is a pressing need to find reliable biomarkers and non-invasive predictors of metastasis and patient response in early squamous cell carcinoma of oral tongue.

Materials/Method: Retrospective analysis was performed in a double-blind manner on tissues microarray (5 cores/patient) created from paraffin-embedded specimens from 50 patients with well documented clinical history of the disease. A subset of 20 different proteins were elected as potential biomarkers of metastasis based on published literature on SCCOT and analyzed through immunohistochemistry. Four proteins, E-cadherin, Podoplanin, Microglobulin and Interleukin-8 were found as possible predicators of metastasis. These findings were validated using Aperio image analysis software.

Results: Digital analysis using Aperio confirmed results for two of the four proteins; E-cadherin and Podoplanin while Microglobulin and Interleukin-8 were found to have non-significant results. Specifically, Podoplanin was found to be upregulated while E-cadherin was downregulated in metastatic patients.

Conclusion: Computer-aided image analysis provides a powerful tool to support clinical decisions while reducing inter-and intra-observer variability. Based on the results from Aperio, Podoplanin and E-cadherin may be used as potential biomarkers to predict nodal metastasis in early tongue cancer. Further studies are required to confirm these findings and to quantify the levels of these proteins in tissue and plasma of patients with cancer compared to non-tumoral controls.

PP56 - The Ig0 domain of Basigin variant-1 stimulates IL-6 expression in RAW 264.7 monocytes

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There are two main protein products of the Basigin gene. One protein, known as Basigin-variant-1 is expressed in the neural retina, specifically by the photoreceptor neurons. The other protein, known as Basigin-variant-2 is expressed throughout the body, including monocytes, as well as Müller glial cells and the retinal pigmented epithelium of the eye. A study by this laboratory indicates that the two Basigin gene products interact via their extracellular domains. A different study by another research group indicates that the Ig0 domain of Basigin-variant-1 can elicit an immune response in several cell lines. The purpose of the present study was to determine if the region of the Ig0 domain of Basigin-variant-1 thought to interact with Basigin-variant-2 is the same region that elicits an immune response. Recombinant versions of the Basigin-variant-1 Ig0 domain were incubated with mouse monocytic RAW 264.7 cells. After 24 hours, the cell culture medium was collected and assayed for the expression of the pro-inflammatory cytokine interleukin-6 (IL-6) via an ELISA. Cells treated with a control protein generated from the expression vector used to make the Basigin-variant-1 recombinant proteins served as the control. The data indicate that the region of the Ig0 domain used to interact with Basigin-variant-2 does indeed stimulate production of a significantly greater amount of IL-6 than the control protein. The data suggest that Basigin-variant-1 interacts with Basigin-variant-2 to stimulate a proinflammatory response in monocytes. This study is important for a better understanding of immune response aspects of diabetic retinopathy and other diseases in which the retinal pigmented epithelium is compromised.

PP57 - Does excess Vitamin B12 affect gene expression and vesicle trafficking in SHSY5Y cells?

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B-vitamin consumption, such as Vitamin B12, has been increasing in the form of energy drinks, vitamin waters, and supplements in recent decades. Little research has been dedicated to high levels of Vitamin B12 as the research has centered on low Vitamin B12 and neurotoxic homocysteine levels that are generated from low Vitamin B12. Interestingly, at the same time as Vitamin B12 consumption increased, neurological diseases such as Autism Spectrum Disorders (ASD) have increased exponentially. Currently, 1 in 59 children is diagnosed with ASD. ASD is a disorder that involves epigenetics, genetics, and neurobiology changes that lead to behavioral patterns like decreased sociability and increased repetitive behaviors. These behavioral changes are rooted in neuronal communications involving vesicle trafficking along microtubules using dynein and kinesin as molecular motors. Tau protein stabilizes microtubules, but if Tau is hyperphosphorylated, microtubules are destabilized leading to disrupted vesicle trafficking. Studies on low Vitamin B12 have shown negative effects on expression of proteins CDK5 and PP2A that phosphorylate and dephosphorylate Tau, respectively. Vitamin B12 has the potential to affect gene expression since it assists with the one carbon metabolic pathway where folic acid becomes a methyl group to affect epigenetic marks on DNA and histones. Therefore, we investigated whether excess Vitamin B12 affects gene expression and vesicle trafficking in a neurobiological model, the SHSY5Y cell. We investigated expression of two motor proteins, dynein and kinesin, as well as levels of Tau protein, phosphorylated Tau, CDK5 and PP2A. We also evaluated vesicle trafficking along microtubules. More research is necessary into the potential effects of Vitamin B12 overconsumption.

PP58 - Determining which G protein-coupled receptors play a role in activating MAP kinases in the presence of various antipsychotics

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This study examines MAPK activation in cells when antipsychotics are combined with different receptor antagonists. Antipsychotic drugs are effective at reducing the symptoms of mental disorders like schizophrenia, yet the mechanisms by which they work inside human cells is not well understood. It is also not well understood why certain antipsychotic drugs work for some people with these disorders and not others. It is already seen in the literature that cells treated with antipsychotics exhibit activation of MAP kinases (MAPKs), which are an important group of intracellular signaling molecules involved in cell survival, proliferation, and stress responses. The question remains of how the drugs are activating MAPKs. To better characterize this activation, fibroblast cells were treated acutely with different antipsychotic drugs (chlorpromazine and clozapine) for a range of time points from 2 to 20 minutes. Western blot analysis has revealed significant MAPK activation at multiple time points. To further address the mechanism of this activation, currently we are working to determine what cell surface receptors may be involved in mediating this response. Specifically, we are repeating the same antipsychotic treatments in combination with different antagonists to block individual receptors. This study will provide new information on how these antipsychotic drugs work inside human cells.

PP59 - *In vivo* Assay to Investigate Sodium Ion Modulation During Inflammation

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Elevated sodium ion levels play an important role in providing a pro-inflammatory environment that induces the chemotaxis of macrophages and upregulates cyclooxygenase 2-activity. Presently, there is no assay to evaluate the extent to which variable sodium ion levels regulate inflammation. Some quinoline-derived compounds are known to possess anti-inflammatory activity, potentially through sodium ion modulation. In this study, we conducted an *in vivo* assay to investigate the modulating effect of five novel quinoline-derived compounds on sodium ions during injury-induced inflammation. After being treated with the quinoline-derived compounds, zebrafish (*Danio rerio)* larvae were stained with CoroNa™ green dye, which enabled the fluorescent visualization of sodium ions. Each larva then received a tissue injury (a needle prick) at the trunk. Sodium ion distribution at the site of injury was recorded pre-injury and every few minutes post-injury. We predicted that the quinoline-derived compounds would result in the inhibited release of sodium ions. Out of five quinoline derivatives, only quinoline-derived compounds 2 and 3 displayed a significant reduction in sodium ion release—comparably less green fluorescence at the site of injury. Compounds 2 and 3 may possess anti-inflammatory and analgesic activities, posing them as potential alternatives to current non-steroidal anti-inflammatory drugs (NSAIDS) and addictive opioids. To further investigate the anti-inflammatory potential of quinoline-derived compounds 2 and 3, we will evaluate their effect on the chemotaxis of macrophages to a site of injury and on cyclooxygenase 2-activity.

PP60 - Analyzing the ability of amodiaquine to function in combination with starvation and additional chemotherapeutic compounds

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Cancer is a highly adaptive disease that is diagnosed in about a third of people during their lifetime. Drug repositioning is an effective and efficient way to explore treatments for existing drugs. Amodiaquine, an anti-malarial, has been shown to inhibit the growth of cancer cells and the ability to synergize with Hanks Balance Salt Solution (HBSS) in melanoma cells. Here, we show that lower concentrations of amodiaquine also acts synergistically with HBSS in MDA-MB-231 cells. Conversely, higher concentrations of amodiaquine behaved antagonistically when combined with Etoposide, a topoisomerase inhibitor, in both MDA-MB-231 and HCT116 cells. These data provide

further details into amodiaquine's mechanism of action as well as contribute clues to other possible chemotherapeutics that will behave interact with amodiaquine.

PP61 - Effect of amodiaquine on gene expression and apoptosis in colorectal cancer cells

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Colorectal cancer has relatively low survival rates. Current treatment options for this cancer still lack efficacy, so there is a demand for new and different drug therapies. Amodiaquine is an antimalarial drug that shows evidence of anti-cancer properties, and it has been shown to reduce cell viability in colorectal cancer cells. Here, we show that amodiaquine is most likely reducing cell viability by inducing apoptosis. Our data shows that of 20 upregulated genes in amodiaquine-treated HCT116 cells, 11 were either pro-apoptotic or DNA damage repair genes. Furthermore, a western blot was conducted and showed cleaved PARP protein, which provides evidence that apoptosis is occurring in amodiaquine-treated HCT116 cells. These data suggest that amodiaquine may be a possible treatment option for colorectal cancers.

PP62 - Anti-proliferative effects of amodiaquine on multiple cancer cell types

Spenser Johnson, Chris Barton

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Cancer is one of the leading causes of death in the United States and current treatments are still not sufficient to prevent high numbers of cancer deaths. While identifying new forms of anti-cancer drugs is important, there are current drugs that can be repurposed to treat cancer in a cost-effective manner. Here, we show that amodiaquine, an anti-malarial, can possibly be used as an efficient anti-proliferative cancer therapy. Our data shows that amodiaquine administered to cervical, lung, and breast cancer cells in vitro demonstrates cell death by apoptosis. This data suggests that the repurposing of drugs to treat multiple types of cancer is an important field within research.

PP63 - Apoptotic effect of amodiaquine on HCT116 colon cancer cells

Sandra Tomas, Chris Barton

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Amodiaquine is an antimalarial drug that has shown promise as an anticancer treatment. Previously, our laboratory identified that amodiaquine is highly effective at reducing the viability of a number of cancer cell types grown in culture. However, the mechanism behind this reduction in cell viability is currently unknown. In this project, we hypothesized that amodiaquine blocked cellular growth through the induction of a caspase-independent apoptotic signaling program. Our data suggest that exposure to amodaquine is sufficient to activate caspase enzymes and induce apoptosis in HCT116 colorectal cancer cells. These data provide mechanistic insight to how amodiaquine is functioning as an anticancer therapeutic. Further experiements are underway to determine whether this drug functions similarly in other forms of cancer

PP64 - Role of P311 in Brown Adipogenesis

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Obesity rates are rising globally, with 1.5 billion overweight and 500 million obese worldwide. According to the Centers for Disease Control and Prevention, almost two-thirds of the United States population is either overweight or obese. Further, growing obesity rates in children and adolescents with one-fourth affected makes the obesity pandemic more alarming and solutions more critical. Obesity increases the risk for insulin resistance, diabetes mellitus, dyslipidemia, hypertension, cardiovascular disease, sleep apnea and certain types of cancer. Current obesity management options – including lifestyle modification, behavioral interventions and invasive surgeries – have met with limited success. Adipose tissue includes white fat/adipose tissue (WAT) and brown adipose tissue (BAT), both endocrine organs that contribute to systemic metabolic regulation. Understanding the adipocyte differentiation of WAT from BAT, as well as the browning of WAT and the whitening of BAT, has many implications for understanding metabolic health and diseases and developing novel therapeutic approaches. Various cellular events and factors, including transcriptional factors and cofactors, regulate mesenchymal stem cell commitment and the differentiation of progenitor cells into preadipocytes and adipocytes. The objective of this study is to elucidate the biology of P311 in brown adipocyte development.

PP65 - Developing Solid-State Nanopore Sequencing for the Detection of Polyelectrolytes on Ocean World Analogs

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Life detection technology suitable for space flight has become a priority due to the proposed Enceladus and Europa missions. Prospective samples collected during these planned missions provide opportunities to search for biosignatures, specifically, polyelectrolytes. DNA and

RNA are polyelectrolyte molecules currently used as biosignature molecules on Earth. Polyelectrolytes act as templates for replication and are potentially necessary for life. Biological based nanopores are not ideal for long term space missions due to the denaturing of protein-based membranes on long duration space missions. Solid state nanopore technology has been proposed as a potential alternative to biological based nanopores. Our research objectives were to 1) determine the solid-state nanopore's ability to maintain a stable baseline in artificial seawater (ASW) and an Icy World analog (Lake Untersee); and 2) test the solid-state nanopore's capability of detecting λ DNA under these conditions. The samples were ASW pH 7.58 and 8.19 and Lake Untersee anaerobic filtered (pH 8.19) and unfiltered water (pH 7.55). Each sample was analyzed without λ DNA to establish a consistent baseline prior to analysis with λ DNA. Larger baselines and clumping of translocations were observed in all samples with higher pH values. We also observed oscillations in the baselines prior to all translocation events. These preliminary results suggest that the solid-state nanopore is capable of detecting λ DNA in artificial seawater at a range of pH values and in environmental samples. Our preliminary results indicate that solid-state nanopores have potential use in detecting polyelectrolytes on ocean worlds and that further refinement of the methods are necessary.

PP66 - Defining the Louisiana Freshwater Sponge diversity with COX1-R1, COX1-D2 Barcoding: A Database Development Study for Classroom Curriculum

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DNA barcoding of freshwater sponges has proved to be difficult for students due to the limited sequences found in the NCBI database. This difficulty stems from the inconsistent use of primers in the literature and the lack of dissimilarity in the targeted genome. The primers chosen for this study were COX1-R1 and COX1-D2. These target the cytochrome oxidase gene and an extension intron that provides variability to differentiate organisms at the species level. To contribute to the database, 147 freshwater sponge samples were collected in a Louisiana survey. The sponges were initially identified based on their spicule and gemmule morphology using standard light microscopy and SEM. Forward and reverse sequences were aligned using MEGA software to provide sequences to deposit in the database. This study provides reference sequences for the most commonly found freshwater sponges in Louisiana: *S. lacustris*, *E. fragilis*, *T. horrida*, *H. baileyi, A. argyrosperma*, *R. ryderi*, *S. alba*.

PP67 - Saffron (Crocus sativus) extract has anticancer activity through inhibition of migraton and invasion potential of breast cancer cells

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Introduction: Saffron is a spice which has been used throughout history for various therapeutic properties. Recently, it has also been documented to have significant anticancer effect on primary tumors. However, limited studies are found studying its effect on metastatic potential of cancers. The goal of our study was to explore the effect of saffron on migration and metastatic potential of breast cancer cells.

Methods: MDA468 breast carcinoma cells were treated with varying concentrations of Saffron and examined using Q-phase holographic time-lapse microscopy to measure the movement of cells over time. The anticancer activity of Saffron was confirmed using cell viability assays. Invasion and metastatic potential was studied using boyden-chamber and scratch wound assays. Finally, tumorigenicity of the cell line was examined through colony formation assays in the presence and absence of Saffron.

Results: Q-phase microscopy revealed reduction in projections and significantly reduced movements in cells after Saffron treatment. The inhibition of migration, cell mobility and invasion by Saffron was confirmed in scratch wound and boyden chamber assays ($p<.05$). Saffron extract also resulted in inhibition of viability in a dose-dependent manner and colony formation assays found markedly reduced size and number of colonies in the presence of the extract.

Conclusions: Our results found saffron to be effective in decreasing breast cancer carcinoma cells MDA468's viability, migration, and tumorigenicity. Future studies will examine its mechanism of action and will focus on delineating the pathways involved in its anticancer effects.

PP68 - The Effects of Bisphenol-S and Bisphenol-F on Breast Cancer Progression

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Estrogen receptors are a group of proteins found in cells that are activated by the estrogen hormone. Endocrine-disrupting chemicals (EDCs) can be naturally occurring or synthetic compounds that have the ability to alter endocrine functions by either blocking or mimicking hormone receptors such as the estrogen receptor. An example of one of these EDCs is Bisphenol-A (BPA), which is found items like food packaging products and electronics. Exposure to estrogen mimics can lead to an increase in estrogen receptor activation. Research has shown that this increase can cause the development of pre-cancerous mammary lesions and breast tumors, resulting in restrictions on BPA and the development of alternatives such as bisphenol-S (BPS) and bisphenol-F (BPF). These alternatives possess similar chemical structures and show similar estrogenic activity as BPA. Recent *in-vitro* studies have shown that BPF and BPS can increase cellular proliferation and migration in the human breast cancer cell line MCF7. From these results, we hypothesized that BPS and BPF will increase tumor progression in human breast cancer. To test this hypothesis, estrogen receptor positive T47D breast cancer cells were treated with 0.1μM BPS or 1 μM BPF for 96 hours. Cellular viability assays demonstrated a significant increase in proliferation and no change in cellular death in cells treated with either 0.1μM BPS or 1 μM BPF when compared to untreated and vehicle controls. We are currently using Transwell ® cell culture inserts to determine if BPS and/or BPF will increase migration and invasion potential in T47-D cancer cells.

In addition, we are using Real-time RT-PCR to determine if BPF and/or BPS can induce an epithelial-to-mesenchymal transition (EMT) by investigating EMT-associated genes. For our future studies, we will investigate the effects of BPF and BPS *in-vivo* by microinjecting the T47D cells into zebrafish embryos and using microscopy to detect metastasis.

PP69 - Production of Competent Cauliflower Protoplast

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Cauliflower (Brassica oleracea) is a useful subject in the field of plant mitochondrial and other biochemical studies as a large part of the plant is colorless. The cells of the cauliflower can be broken open to isolate specific organelles without chlorophyll contamination. Repeatedly buying cauliflower plants introduces a large number of variables into every study. Very few reports on the culture and growth of cauliflower cells in the lab exist. This experiment seeks to develop a protocol for the lab culture and production of cauliflower cells for use in further plant studies. A liquid culture was the method chosen as many studies performed require cells rather than tissues. The protocol describes the disinfection and collection of cells from a store-bought cauliflower plant. The cells were then placed into the liquid culture based on Murashige and Skoog's growth and culture media. The media also contains gibberellic acid to induce the growth of the growth of the apical meristem cells of the cauliflower (otherwise known as the 'curd'), pre-mixed W5 solution to produce protoplasts of the plant tissue, as well as an auxin. Three auxins of varying concentrations were tested for efficacy— 3-indoleacetic acid (IAA), indole-3-butyric acid (IBA), and 1-naphthaleneacetic acid (NAA). The cell cultures were then incubated on a rotary shaker at 27 C and periodically sampled under a microscope to quantify health and growth. Visual tests were then performed on the protoplasts using vitality stains, as well as biochemical tests to further examine protoplast viability in other experiments.

PP70 - Temporal and spatial overlap of margays (*Leopardus wiedii*) and their potential prey

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The margay (*Leopardus wiedii*) is a small, near threatened neotropical cat. Its diet consists of small mammals, birds, amphibians and lizards. We compared the temporal and spatial activity of margays and their potential mammalian and avian prey via camera traps deployed in Wildsumaco Wildlife Sanctuary, Ecuador. Potential prey species captured include numerous bird species, small rodents, squirrels and opossums. The margays were largely nocturnal and had the largest spatial overlap with squirrels, followed by small rodents and birds. The species with the greatest temporal overlap with the margay are rodents who also display nocturnal behavior.

PP71 - Comparison of Bird Diversity Reported at an eBird Hotspot and A Banding Station in an Urban Natural Area Park in Nashville, Tennessee

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Belmont University, Nashville, TN

Data from eBird were used to compare the diversity of birds reported by citizen scientists to the diversity of birds banded in the same area. The Warner Parks in Nashville, TN have both a public and banding eBird hotspot in close proximity. Data from the public hotspot (=observed) and the banding station (=banded) from May 2008-2018 were obtained from eBird. During this time period, 15,622 birds were observed (142 species), while only 9,099 birds (58 species) were banded. Simpson and Shannon indices suggest that diversity was greatest among the observed community. Jaccard's Coefficient of Community Similarity indicates that 57.93% of the species occurred in both the observed and banded datasets. The most commonly banded and observed families were the Paridae, Turdidae, and Cardinalidae. Citizen science data may not be as complete or accurate as banding data. Banding provides more detailed information about birds but may not reflect the full diversity of birds in a given area unless a variety of banding techniques are intentionally employed. Overall, the data reinforce the importance of the Warner Parks as an important bird habitat in an urban natural area park.

PP72 - The effects of night time light pollution on insect abundance and community composition

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Davidson College, Davidson, NC

Many insects rely on light to provide cues for behaviors involved in reproduction, foraging, and navigation. However, human-produced light at night may cause inappropriate behaviors or physiological responses, leading to extended activity of diurnal insects or attraction to light sources in both diurnal and nocturnal insects. Given the expansion of artificial light at night (ALAN), we examined the effects of ALAN on insects. We collected data on insect communities and abundance of particular taxonomic groups using light traps over two consecutive summers. Light traps were constructed with an ultraviolet light installed in front of a white sheet hung on a PVC pipe frame at 6 sites on a suburban college campus: three sites continuously lit at night and three dark sites. Data were digitally recorded using a high resolution DSLR camera so that the insects could be identified and quantified later. Physical specimens were also collected as needed for identification. We found that total insect abundance increased significantly as temperature increased in the dark sites, and this rate of increase was significantly greater than than the much smaller increase with temperature at lit sites. Moths, scarab beetles, rove beetles, mating ant swarms, and a group of small unidentified insects were significantly more abundant at dark sites than at lit sites, with several of these groups also increasing their activity with temperature. These groups of insects each have important ecological functions, including pollination, decomposition, predation, and food for predators. We conclude that temperature is a strong indicator of insect activity at light traps, but that ALAN significantly disrupts insect abundance, and affects taxonomic groups of insects differentially, thereby likely altering

community composition.

PP73 - The effects of ecological light pollution on an autumn insect community

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Rapid global declines of insects have been linked to an increase in global urbanization, and along with that, the intensification of artificial light at night (ALAN). Many insects rely on light to provide cues for a variety of behaviors involved in reproduction, foraging, and navigation. ALAN may alter or disrupt behaviors or physiological responses, leading to a variety of effects on individuals that could translate to changes in populations and communities. Given the global increase of artificial light at night (ALAN), we sought to examine the effects of ALAN on insects. We established PVC-frame UV light traps at six different locations on a suburban college campus north of Charlotte, NC during Autumn 2019. We collected data from three lit sites and three dark sites each week from the end of August to mid-October. We recorded high resolution digital images of insects that collected on light traps to later identify and quantify the abundances of insects. Compared to stark differences in total insect abundance in two previous summers, where insects were significantly more abundant at dark than at lit sites especially at higher temperatures, we found no statistically significant relationship between total abundance of insects at lit and dark sites and temperature in autumn 2019. However, we did find that lepidopterans had higher abundance at dark sites. The general lack of effect in the autumn of 2019 could have been caused by a different set of insect species becoming active later in the field season, which could have also been related to that different set of species being exposed to an usually warm autumn. While we have documented a large negative effect of ALAN for insects active in the summer, the overall lower abundance of autumn insects and the warm temperatures led to no observed effect of ALAN in this experiment.

PP74 - Consistent spatiotemporal patterns in water mite (*Arrenurus* spp.) parasitism of dragonflies (Order: Odonata).

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Water mites (*Arrenurus* spp.) are common parasites of dragonflies (Order Odonata). Larval mites climb aboard a late instar dragonfly larva, attach to the emerging metamorph, and feed on hemolymph for at least 10 days. They can reach densities of over 400 mites on a single dragonfly and reduce survivorship and fecundity. However, few studies have described the spatiotemporal consistency of water mite parasitism. In summer 2019, we sampled dragonflies from seven waterbodies in Greenville Co, SC, USA that had been sampled in 2014, and compared parasitism rates between sites, between years, and across species. Parasite prevalence (% of hosts infected) did not vary significantly between years (2014: 14.5%, 2019: 16.9%). However, prevalence did vary between sites in both years, ranging from 6.7% - 21.4%. Prevalence rates at sites were remarkably consistent between these samples taken five years apart ($r = 0.942$, $N = 7$, $p = 0.001$), suggesting rather stable populations of water mites. There were no consistent differences in prevalence between species. Rather, prevalence was strongly correlated with the relative abundance of a species at a given site. This suggests that hosts are colonized randomly, and that any differences in larval behavior or ecology may not meaningfully affect susceptibility to parasitism by water mites.

PP75 - Arthropods associated with vegetative and flowering stages of the blue mistflower, *Conoclinium coelestinum* (Asteraceae)

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The blue mistflower, *Conoclinium coelestinum*, is an herbaceous perennial native to the eastern United States. The plant reproduces readily by seed and invasive rhizomes. The persistence of flowers into the fall makes *C. coelestinum* a desirable addition to many gardens and a noteworthy nectar source. In an effort to investigate the potential role of this plant as a refuge for beneficial insects or a source of pest insects in household gardens, we collected arthropod specimens found in association with either the vegetative or flowering stages of *C. coelestinum* in an urban environment over the period of May to November, 2019. We made preliminary genus-level identifications of 54 species of arthropods engaged in a variety of activities including herbivory, predation and parasitism. Some species were identified using barcode regions of the cytochrome oxidase I (COI) gene. The most abundant insect identified on *C. coelestinum* to date is a mealybug (*Planococcus* sp.). This insect, or a closely associated but as yet unidentified aphid species, caused a substantial amount of leaf and flower head damage due either to feeding or virus transmission. These pest insects were consumed by both larval and adult coccinellid beetles (*Scymnus* / *Coccinella*) as well as lacewing larvae (*Chrysoperla* sp.). Despite the extensive damage caused by pest insects, a very robust set of blooms and seed set was observed in the fall. Taken as a whole, our findings suggest *C. coelestinum* could supply either or both pest as well as beneficial insects to neighboring plant species in close garden spaces. Also, the sum total of organisms found in interactions associated with *C. coelestinum* over its growth and flowering seasons permitted sustainable growth of the plant and its likely expansion in the urban environment under observation.

PP76 - Relationship between a reproductive polymorphism in the Spotted salamander and its unicellular algal symbiont

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The spotted salamander, *Ambystoma maculatum,* exhibits a unique reproductive polymorphism wherein some females lay clear egg masses while others lay opaque masses. *A. maculatum* engages in a symbiosis with a unicellular algae, *Oophilia amblystomatis*, that lives intracellularly within the egg envelopes of *A. maculatum* and provides embryos with supplemental oxygen via photosynthesis. Clear

and opaque egg masses often co-occur in breeding ponds, but proportions of egg mass types vary spatially. Our previous work shows that predators preferentially consume clear egg masses so it is perplexing that they persist. Clear jelly may be an adaptation to low dissolved oxygen environments, possibly by allowing for higher light transmittance and thus increased photosynthesis by *O. amblystomatis*. Here, we investigate the relationship between jelly polymorphism, algae symbiosis, and dissolved oxygen through both observational and experimental designs. We sampled *A. maculatum* breeding sites for egg mass proportions, predators, and water physicochemicals. Additionally, we raised clear and opaque egg masses under two different light treatments, sampled embryonic respiration at two developmental stages, and quantified algal growth. Our study elucidates some heretofore unknown differences between the two mass types, such as differential algal growth, clutch sizes, and hatchling viability. Finally, our data suggest that dissolved oxygen may be one selective pressure responsible for maintaining this polymorphism.

PP77 - Vertical layering of animals in forested ecosystems in northwest Tennessee

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Increases in vertical layering of vegetation in ecosystems tends correlate to higher diversity of animals due to increases in available niches. By placing feeders at different heights in the environment, our goal was to observe stratification of animals in forested ecosystems in northwest, Tennessee. We mounted 5 motion sensing cameras 1m above the ground and 5 cameras 3m above the ground. Directly in front of the cameras, we placed feeders baited with suet mixed with seeds, peanuts, and peanut butter. The cameras took a total of 31,190 photos and we were able to identify animals on 1,569 photos taken at 1m and 4,314 photos taken at 3m. We observed six species of mammals visiting 1m feeders and 5 species on 3m feeders. We observed 15 avian species visiting 1m feeders and 19 species using 3m feeders. While birds were observed feeding at both heights, they were photographed most frequently on the 3m feeders. The overall diversity of organisms observed was slightly higher on the 1m feeders. Overall, there was intermediate overlap in species composition between the two communities suggesting that some vertical layering is occurring within the forest. We also observed temporal layering since the majority of mammals visiting the feeders were nocturnal, whereas birds were more diurnal.

PP78 - The Effects of Prescribed Fire on Oak-Forest Plant Communities over 25 Years

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In the Eastern US, fire is a natural process in *Quercus* (oak) forests. Fire promotes oak regeneration by reducing competition, preparing a suitable seedbed, and decreasing soil moisture. However, oak regeneration has declined since the early 20th century due, in part, to fire exclusion. In this study, we examined the effects of fire on tree regeneration over 25 years and asked: (1) Does tree regeneration vary under different fire regimes? and (2) Do the outcomes of prescribed fire (or lack thereof) differ on xeric, intermediate and mesic sites? We re-sampled a study initiated in 1994 to understand the effects of fire frequency on oak-forest plant communities. We re-sampled 45 1250 m^2 permanent vegetation plots across three fire treatments (unburned, annually burned, burned every three years) in two sites in the Wayne National Forest, OH. Pretreatment data was collected in 1995 and low-intensity prescribed burns were conducted during 1996-1999 followed by a mostly fire-free period. In 625 m^2, tree seedlings (all stems <1.4 m tall) were tallied and identified in sixteen 2 m^2 quadrats. Using linear mixed effects models, we examined if seedling density changed from 1995 to 2019 across different fire treatments and with soil moisture. There was a significant increase ($p < 0.01$) in total seedling density/ha on xeric sites in 2019 (mean=63,485) relative to 1995 (mean=27,013). There was no significant change in seedling density on mesic or intermediate sites or between fire treatments. *Quercus, Acer, Sassafras,* and *Fraxinus* seedlings significantly increased ($p < 0.01$) on xeric sites by 2019, while *Fagus* seedlings did not. Mean increases in seedlings/ha for *Quercus* and *Acer* were 8,873 and 31,207, respectively. Our results suggest that seedling density has increased since 1995 on xeric sites, regardless of fire treatment, and fire had little effect on seedling regeneration.

PP79 - Investigation of an indirect defense mechanism of *Chapmannia floridana* in Florida scrub

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Plants have many direct defenses, such as thorns and toxins, which increase their survival and reproduction. Recent studies have shown that some plants have indirect defenses as well, specifically glandular trichomes (i.e., sticky hairs) that entrap carrion, which attract predators that consume the carrion. Predators deter herbivores from harming the plant, leading to an increase in the survival and/or reproduction of the plant. Flowering stems of *Chapmannia floridana* (Florida Alicia), a perennial plant that is endemic to Florida, are covered in sticky hairs, which may act as an indirect defense. We assessed 84 flowering *C. floridana* individuals across six habitats in the Florida scrub ecosystem. We measured the total flowering stem height and the height where trichomes start, counted the number of fruits, flowers, and buds present, and documented any damage to reproductive structures. We also counted the number of carrion, herbivores, and predators on *C. floridana* flowering stems. There was no difference in the length of the trichome-covered portion of flowering stems among habitats. We found a positive correlation between the length of the trichome-covered portion of *C. floridana* flowering stems and the number of carrion trapped. Only 10% of fruits, 15% of flowers, and 19% of flower buds we counted on flowering stems were damaged. We found predators (i.e., spiders) on 6% of flowering stems and herbivores (e.g., grasshoppers, leafhoppers, caterpillars) on 37% of flowering stems. We found no association between habitat and damage (for scrubby flatwoods and firelane habitats only) and no association between carrion presence and damage. However, the probability of damage to reproductive structures decreased as the number of trapped carrion increased. Overall, our results suggest that herbivory of *C. floridana* reproductive structures is relatively low and glandular trichomes on *C. floridana* may be acting as an indirect defense.

PP80 - Urbanization's Impact on Air Quality and its Correlation to Children's Respiratory Health

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Background: In 2017, the Centers for Disease Control conducted a National Health Interview Survey to collect data on asthma prevalence in the United States. The study found that there is a total of 7.9% of people of all ages with existing cases of asthma. The asthma prevalence percentage in children (age<18) was 8.4%. A Fulton County Health Status Report done in 2016 revealed that 17% of children living in Fulton County, Georgia aged 6-11 were diagnosed with asthma during that year. This percentage is double the 2017 national childhood asthma prevalence percentage. The aim of this study is to better characterize the relationship between urbanization, air quality and childhood asthma in the United States.

Methods: National Land Cover maps from the years of 2006 and 2016 were downloaded from the Multi-Resolution Land Characteristics Consortium. GIS mapping was used to home in on Fulton County and analyze the differences in land use between the years 2006 and 2016. Raw air quality data of NO□, O□ and PM 2•5 were downloaded from the Environmental Protection Agency website. Annual AQI averages were calculated for each pollutant every year from 2008-2018. Monthly AQI averages were also calculated for each pollutant from January to December every year from 2008-2018.

Results: Concentrations of NO□ peaked during the colder months (November-February). Levels of nitrogen dioxide significantly increased in developed areas with greater concentrations of medium to high intensity populations. O□ concentrations increase during the hotter months (June-August). Concentrations of PM 2•5 showed little variation throughout the year. In Fulton County, areas of low intensity transitioned to areas of medium intensity and areas of medium intensity developed into areas of a higher intensity. Future work needs to be done to understand the effect of air pollutants on children's respiratory health.

PP81 - Current Plant Community Composition at the Sheffield Wildlife Management Area.

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The Sheffield Wildlife Management Area (WMA), located within the Piedmont ecoregion, was established to provide important wildlife habitat and ensure the protection of the Raccoon Creek watershed. It is currently a mosaic of forests that have experienced relatively light management. However, due to long-term fire suppression, the rare montane longleaf pine ecosystem that used to be present in some areas has been greatly diminished. The goal of this study is to provide baseline data on plant community structure across the Sheffield WMA (and eventually also the adjoining Paulding WMA) to aid in planning and monitoring current and future restoration efforts, as well as help determine the success of those efforts.

Thirty-six plots were set up near the top of ridge lines on either north or south facing slopes. Plots were located in areas where longleaf pine was historically dominant as determined by the presence of old stumps. Each plot was composed of three adjacent 10m x 10m squares parallel to the fall line within which each tree was identified to species and its DBH recorded. Cover of herbaceous species and seedlings/saplings was estimated in six 2m x 2m plots within each larger plot. From this data we calculated relative density, dominance, frequency, and average percent cover. Diameter size class frequencies of longleaf pine will be presented and compared to those of other longleaf pine forests with various management histories. We compared the communities on the two slope aspects and will present the beginning of a comprehensive species list for the whole Sheffield WMA. Results indicate a lack of longleaf pine in the smaller diameter size classes, along with clear differences in the frequency and dominance of various tree species between the two slope aspects. Biodiversity as measured by the Shannon Index was greater on the south slopes.

PP82 - Drivers of mesocarnivore community structure in southcentral New Mexico.

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The relative contribution of top-down and bottom-up forces in structuring ecological communities is of particular interest as populations of apex predators continue to decline worldwide. We used 10 years of remote camera photo data from a 100 Km Sq, permanent grid in southcentral New Mexico to assess the relative contributions of top-down and bottom-up forces structuring the mesocarnivore community. Specifically, we used quantile regression to determine the relative influences of puma (Puma concolor) and black bear (Ursus americanus) – top-down factors – and jackrabbit (Lepus californicus) and desert cottontain (Sylvilagus auduboni) – bottom-up factors – on the diversity of the mesocarnivore community across 25 camera sites. The mesocarnivore community on our study site consisted of coyote (Canis latrans), bobcat (Lynx rufus), gray fox (Urocyon cinereoargenteus), ring-tailed cat (Bassariscus astutus), and badger (Taxidea taxus). Our results indicated that while puma were the primary drivers of mesocarnivore community structure, black bear, and cottontails were also significant factors. Pairwise species comparisons indicated that puma significantly suppressed coyote and bobcat, but were associated with increased gray fox abundance and significantly lower cottontail abundance. It appears that puma alter the mesocarnivore community by releasing gray fox from coyote predation/competition. Lower cottontail numbers associated with puma might be the result of increased gray fox predation or avoidance.

PP83 - A comparison of pollinator assemblages on Helianthus porteri to those on other plant species in a granite outcrop community

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Helianthus porteri is a rare, endemic species of sunflower that grows in granite outcrop communities of the Piedmont region of Georgia. Pollinators visiting *H. porteri* and other flowering plant species in the area were captured during the flowering season of *H. porteri* to determine whether the assemblages of pollinators differed between the two groups. Multiple response permutation procedure (MRPP) did not find a significant difference in assemblage between the two sets of samples. A rarefaction curve based on samples from *H. porteri* was significantly steeper than a curve based on samples from other flowering plants in the area, indicating that this species is an important contributor to local pollinator diversity.

PP84 - Successional dynamics of an Appalachian pin oak (*Quercus palustris* Münchh.) swamp forest

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Bottomland forests provide ecosystem services such as nutrient exchange and pollution entrapment and generally improve aquatic and riparian habitats. In West Virginia, little is known about the development and resiliency of isolated bottomland sites dominated by *Quercus* species, which have declined in area due primarily to draining and development. In this study, we used vegetation surveys and tree-ring analysis to investigate successional dynamics and the timing and drivers of recent overstory mortality in a remnant stand located on the floodplain of the Meadow River. Our results indicate a rapid change in vegetation cover at the site between 2011 and 2017, with a significant decrease in tree canopy cover and an increase in light-demanding, flood-tolerant herbaceous species cover. Historical trends in tree establishment indicate an absence of *Quercus palustris* recruitment after the 1960s and an increase in the recruitment of *Acer rubrum* and other shade-tolerant species. Furthermore, temporal trends in hydroclimate-tree growth relationships suggest that an increasingly temperate climate and higher water table benefited *A. rubrum* at the expense of *Q. palustris* beginning in the 1990s. Taken together, these findings suggest a gradual, multi-decade, process of plant community reorganization beginning in the mid-20th century. This process might have continued unabated, but flooding and persistent high water in 2003 amplified the wetting trend and initiated the progression of widespread overstory mortality. Our results suggest that *Q. palustris* forests in the Meadow River wetlands are maintained by infrequent stand-replacing disturbances, but the current long-term wetting trend could create site conditions unfavorable to tree growth. Furthermore, these findings highlight the need for additional analysis of bottomland vegetation dynamics in the Appalachian Mountains, where increased hydroclimate variability, including extreme flooding, is predicted.

PP85 - Ground Layer Vegetation Response to Oak Regeneration Treatments in Southern Appalachian Forests

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Southern Appalachian forests contain unique microhabitats for ground layer vegetation species due to their varying topography and geologic history, among other characteristics. There are several hundred state-listed and many federally listed species of concern in North Carolina, many residing in the Southern Appalachian region. Ground layer species also play an important role in ecosystem functions such as seedling regeneration, nutrient cycling and wildlife resources. Consequently, the retention or restoration of species composition and diversity of the ground layer vegetation community has been a growing concern for researchers. Silvicultural management techniques developed to promote oak regeneration are often used in Southern Appalachian forests. It is important to consider the consequences that species-targeted management techniques have on the growth, survival and diversity of the ground layer vegetation community. As part of a larger “Regional Oak Study” being conducted by the US Forest Service in the Cold Mountain Game Lands of western North Carolina, the objective of this study is to compare how silvicultural management techniques, such as repeated prescribed fire (RxFIRE), oak shelterwood harvesting with herbicide (OSW), or shelterwood harvesting followed by prescribe fire (SWF), affect the growth and survival of the ground layer vegetation community. We hypothesize prescribed fire treatments (SWF and RxFIRE) will promote greater biomass production by increasing available light following canopy and fuels reduction post-fire. We further hypothesize that species composition will shift from more shade-tolerant, fire-sensitive lifeforms (HERBS, FERNS) to more shade-intolerant, fire-resistant lifeforms (SHRUBS, VINES) in the SWF and RxFIRE treatments. We are testing the effects of treatments on repeated measurements of ground layer species cover and richness over a decade following initial treatment establishment. We will use multivariate analyses to evaluate the treatment versus habitat effect on lifeform biomass potential and to evaluate long-term changes in lifeform cover in response to the silvicultural treatments.

PP86 - Determining the Most Effective Planting Strategy for Dune Restoration on Tybee Island

Shannon Matzke

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Tybee Island has begun large-scale dune restorations along its beaches; however, no studies have been conducted to determine best practices for these restorations. We are conducting a study to experimentally evaluate the results of four different restoration treatments, focusing primarily on the most effective revegetation methods for the desired outcomes- sand accumulation and stability.

At the completion of dune construction in January 2020, we will establish six replicates of two different assemblages of dune-building grasses and typical foredune forbs in low and high planting densities to create four restoration treatments in the newly constructed dune across approximately 900m. Assemblage 1 will be based on the current plant composition of pre-existing dunes, and Assemblage 2 will be

determined based on best planting practices from other restorations. These treatments will be compared with each other, with unvegetated sites on the constructed dune (control 1), and with a pre-existing healthy reference dune (control 2), in order to evaluate best practices that support optimal plant growth and the maximum sand binding capacity required to maintain dune elevation and vegetation cover.

Five randomly selected m^2 quadrats will be established in each replicate treatment and control for repeated sampling for a total of 180 quadrats. Aboveground vegetation data and accretion data will be collected 2-4 times a year based on growing season. Vegetation biomass data will be collected one year after completion of revegetation.

The objectives of this study will be to assess how well the current dune restoration projects restore ecological function to degraded areas of beach and build lasting dune structure that will provide ecosystem services to both the natural and human residents of Tybee Island.

We will present an overview of the planting assemblages and a layout of completed revegetation along with baseline vegetation data from existing and previously revegetated dunes.

PP87 - Changes in adult odonate communities along the Reedy River in Greenville Co., SC: habitat associations at several spatial scales

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Anthropogenic habitat change can have positive and negative effects on dragonflies (Order: Odonata). We sampled 10 2m x 2m subplots in 2 plots at 15 sites along the Reedy River in Greenville Co, SC, from headwater sites through suburban and urban landscapes. We measured aquatic substrate characteristics, bank vegetation characteristics, light conditions, water temperature, pH and conductivity, and quantified the % cover of different landforms within a 500m radius of each plot using GIS. We sampled adult dragonflies three times in each subplot, and computed abundance, species richness, and Simpson's diversity for damselflies, dragonflies, and all odonates at subplot, plot, and site scales. We used AIC modeling to determine which independent variables were the best predictors of our nine community indices at each scale. At the subplot level, site identity and % cover of sunshine in subplots were the best predictors of all nine indices. At the site scale, damselfly abundance was negatively related to total forest cover and medium development, whereas richness and diversity simply increased downstream. Dragonfly abundance was positively associated with the mean % cover of rooted macrophytes and total wetland area, while dragonfly richness and diversity were negatively associated with total developed area and open developed area, respectively. Damselfly communities were affected more by variation in sunlight and downstream changes in general river parameters, whereas dragonflies were more negatively affected by anthropogenic habitat transformation to the surrounding area.

PP88 - Temporal and spatial patterns in barnacle colonization on *Spartina alterniflora*

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Spartina alterniflora is the dominant plant species of coastal salt marshes along the East Coast of the United States and plays a pivotal role in salt marsh maintenance, growth, and primary production. Significant colonization of *Chthamalus fragilis* has been noted along the leaves and stems of *S. alterniflora* within Georgia salt marshes, subsequently raising questions concerning the impact of this colonization on *S. alterniflora* communities. The purpose of this study was to determine if temporal and/or spatial patterns exist in *C. fragilis* colonization on *S. alterniflora*. *C. fragilis* colonization on stems and leaves of *S. alterniflora* was assessed through a field survey for randomly selected *S. alterniflora* individuals within three salt marshes of varying marine influence in June and July 2017 and 2018. Results showed significantly more *C. fragilis* on leaves and stems in 2018 compared to 2017, as well as significantly more *C. fragilis* settlement in the month of June compared to July, suggesting both annual and monthly patterns in colonization. Furthermore, a positive relationship was found between proximity to the ocean and *C. fragilis* occurrence on *S. alterniflora*, indicating spatial patterns in settlement. The annual and monthly patterns of settlement observed in this sutdy may be correlated to *C. fragilis* reproduction and/or larval survival, while spatial patterns may be correlated to environmental conditions favoring larval recruitment. Further investigation of *C. fragilis* reproduction and larval recruitment is needed to elucidate the influence of seasonal and environmental factors on *C. fragilis* settlement on *S. alterniflora*.

PP89 - The role of host availability in maintaining oak mistletoe (*Phoradendron leucarpum*) in forested wetlands of eastern Virginia and North Carolina

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The oak mistletoe (*Phoradendron leucarpum*) is a parasitic shrub found across the southern United States growing on deciduous trees. Among forested habitats of eastern Virginia and North Carolina, mistletoe is most common in forested wetlands despite the widespread occurrence of potential host tree species. Mistletoes are considered keystone resources and, thus, oak mistletoe is likely an important resource for avian frugivores wintering in forested wetlands of the region. It is important to understand processes that maintain mistletoe in forested wetlands, yet the factors most influential in driving oak mistletoe habitat relationships remain unidentified. Host tree availability has been proposed to be responsible for the association between oak mistletoe and forested wetlands in the region. We collected data on the occurrence of mistletoe at 96 plots in either forested wetlands or forested uplands across eastern Virginia and North Carolina. Percent canopy cover and density of tree stems were recorded at each plot. Data on parasitized tree identity from plots containing mistletoe was combined with such data from ad-hoc forested sites across the region. A principal components analysis was used to identify clusters representing geographic host associations, and host tree availability was calculated at each of the plots using a plot-specific list

of potential host species based on its location. Mistletoe occurrence data at the plots was then analyzed using a generalized linear model to estimate the effects of habitat and the availability of light and host trees on occurrence rate. A significant positive relationship between forested wetland habitat and oak mistletoe occurrence was found after controlling for the other variables, suggesting another factor such as dispersal limitation may play an important role in determining mistletoe habitat relationships in the region.

PP90 - Response of foraging birds to playback of calls from a non-bird eating hawk and a bird eating hawk at feeding stations in northwest Tennessee

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Recognizing potential threats can influence the energetic demands, and therefore the survival of wintering birds. Reacting to sounds that are not a threat wastes time and energy that could be spent foraging. Our goal was to determine if birds visiting feeding stations were more likely to flush upon playback of calls from a non-bird eating hawk (non-threat) as compared to the call of a bird-eating hawk (threat). Observations were made at four feeding stations, each consisting of a blind with tube and platform feeders regularly baited with black oil sunflower seeds. Two of the feeding stations were located in upland hardwood forests and two in bottomland hardwood forests. We used a Bluetooth speaker paired with a smartphone to project calls using the Merlin Bird ID application. We played the calls of a Red-tailed Hawk (*Buteo jamaicensis*) as a non-threat and the calls of a Cooper's Hawk (*Accipiter cooperii*) representing a potential threat. We allowed the feeders to populate with birds and then counted the number of individuals of each species. Once the feeders were populated we played one of the hawk calls. Following playback, we counted the number of birds present at the feeders. Our preliminary results indicated that the mean number of birds present after the playback of Cooper's Hawk calls was significantly less than the number of birds present before playback. There was no difference in the mean number of birds present before and after playback of Red-tailed Hawk calls, suggesting that songbirds may be distinguishing between the calls of bird eating and non-bird eating hawks.

PP91 - Patterns of Chinese privet (*Ligustrum vulgare*) invasion and beaver browsing damage in a recently restored wetland on the campus of Piedmont College (Demorest, GA)

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The area surrounding nine water-level monitoring wells, in a restored wetland on the campus of Piedmont College (Demorest, GA), were surveyed for Chinese privet (*Ligustrum vulgare*) cover and tree damage by beavers. We were interested in the influence of water-level on Chinese privet cover, of tree species on beaver browsing, and of location within the wetland system on both. Privet occurred at four out of nine sites and there was no consistent relationship between water-level and cover/occurrence. The four locations with privet were all along the upstream boundary to the wetland, which suggests that privet cover is related to other factors than water level, such as history and human activity. Beaver damage was related to location, with three out of 10 locations having damage, but was not species-specific. The three locations with damage were all in close proximity to a large beaver pond.

PP92 - Characterizing winter herbivory in cranefly orchid, *Tipularia discolor* (Orchidaceae)

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Leaves of cranefly orchid, *Tipularia discolor,* exhibit a striking range of leaf color phenotypes. Adaxial surfaces of leaves may bear silver flecks, purple spots, solid purple coloration, or a combination of two or more of these features simultaneously. Our current hypothesis is that these leaf markings function as an herbivory deterrent or camouflage, since cranefly orchids produce only one to two leaves per year. The objective of this study was to characterize seasonal herbivory in a natural population of cranefly orchids exhibiting three (2018-2019) and five (2019-2020) different leaf phenotypes. Studies took place at the Piedmont Environmental Center in Jamestown, NC. We tracked over 900 hundred orchids, visiting leaves on 2-3 week intervals over the growing season to monitor changes in herbivory. Any arthropods or other organisms observed on leaves were captured, preserved in ethanol, photographed under a microscope, and identified by members of iNaturalist community. Results showed that the most common types of herbivory (in order from most to least common) were: complete removal of the leaf (likely by deer), small (<2 mm) round holes within the central part of the leaf, truncated/nipped leaf tips, leaf miner damage, and feeding at the leaf margin. The purple-spotted leaf phenotype was most abundant at the field site, and also incurred the most whole-leaf herbivory in the 2018-2019 field season. However, when normalized by number of individuals, percent defoliation was highest in green leaves, followed by spotted, and then purple leaves, consistent with an herbivory defense function of purple spots and color. Potential herbivores directly captured or observed on leaves during the 2018-2019 field season included slugs, snails, and leaf hoppers. Several species of spiders were also observed occupying *T. discolor* leaves during winter, including jumping spiders and several species of orb-weavers. We are currently collecting data for the 2019-2020 field season.

PP93 - Assessing the effect of eastern hemlock decline from hemlock woolly adelgid infestation on mycorrhizal fungi

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Eastern hemlock (*Tsuga canadensis* L.) is a foundation species in eastern North American forests, providing critical habitats for a number of species. Hemlocks are experiencing widespread decline due to the spread of hemlock woolly adelgid (HWA: *Adelges tsugae* Order Hemiptera) into their range, potentially resulting in the functional disappearance of hemlocks from eastern forests. Hemlock dieback leads to cascading effects on associated ecosystems, including below-ground, mycorrhizal fungal communities. Mycorrhizal fungi, which

are mutualistic with many plant species and provide nutrients to plant hosts, have been shown to colonize hemlock and neighboring tree species at lower rates following HWA infection. This study investigated the effect of hemlock decline from HWA infestation on the mycorrhizal community. Hemlock health surveys were conducted in healthy (Carl Sandburg Home National Historic Site – CARL) and declining (Warren Wilson College – WWC) stands in western North Carolina and paired trees (based on diameter) in each stand were selected. In each stand, northern red oak (*Quercus rubra* L.) "bait" seedlings were planted within a meter of "host" hemlock trees in early summer and allowed to grow for eight weeks, when they were harvested. Seedling growth and dry biomass were recorded at harvest and roots were sampled for mycorrhizal colonization rates. Different mycorrhizal morphotypes were collected for DNA extraction to compare mycorrhizal community assemblages between the two stands. Both oak seedling height and mycorrhizal inoculation rate were significantly greater in the healthy hemlock stand (CARL) than in the declining stand (WWC), suggesting that healthy hemlock stands are more favorable for oak seedling growth than declining stands. We are currently using DNA barcoding to determine if changes in mycorrhizal community composition associated with hemlock decline might be a factor in poorer seedling performance in declining stands.

PP94 - Detection and Identification of Arbuscular Mycorrhizal Fungi and Surrounding Microbiome in Two Riparian Tree Species

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This research forms part of a larger project investigating the feasibility of using American Sycamore (*Platanus occidentalis* L.) in addition to Black Willow (*Salix nigra*Marshall) in restoration of riparian areas. Riparian vegetation functions in the regeneration of ground water sources, in the removal of excess nutrients and sediments from surface runoff, and in maintaining favorable environmental conditions for life in this system.

Preliminary studies in our lab comparing the two riparian species, found that although both were colonized by arbuscular mycorrhizal fungi (AMF); the rates of colonization, as quantified under the microscope, differed among both species. In addition, recent research suggests that the plant root microbiome may play an important role in plant health and well being and that plants may be able to influence their root microbiome, recruiting beneficial microorganisms and suppressing pathogens.

We hypothesize that both riparian species will be colonized by the same AMF types, but will differ in other aspects of their microbiome community. To identify AMF within each plant root and establish whether samples came from each plant species, we extracted DNA from root samples using theDNeasy Powersoil Kit (Qiagen). For the identification of AMF after DNA extraction, we targeted the small subunit of rRNA genes using AML1 and AML2 primers to amplify and distinguish among subgroups of *Glomeromycota*fungi. To identify the host plant DNA, a similar protocol was ran using AB101 and AB102 primers. The electrophoresis gels showed that most of our samples had very pronounced bands of amplified AMF DNA but had very faint or no bands of plant DNA. The microbiome results showed similar percent colonization of certain phyla among both species. The next step in our research is to distinguish the types of AMF in our sample roots and to repeat amplification of our plant DNA.

PP95 - Response of Chestnut Hybrids to Forest Management Strategies in West Virginia

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The American Chestnut (*Castanea dentata*) was once a co-dominant canopy species in Eastern forests of the United States. A pathogenic fungus *(Cryphonectria parasitica)* decimated this tree species to functional extinction over sixty years ago. Our research attempts to identify forest management strategies for increasing the success of hybrid chestnut (BC_3F_3 generation) plantings in forested ecosystems. We manipulated factors that may facilitate seedling survival and growth in an Appalachian cove forested ecosystem in West Virginia. We created canopy gaps of different sizes (40% vs 60% canopy openness) to manipulate light with the prediction that seedlings would perform best in larger gaps. Within these gaps, we added landscape fabric on every other row to decrease vegetative competition. We placed 12" tree shelters around half of the seedlings planted within the gaps to protect them from rodent predation. All gaps were surrounded by deer fences. After five years, seedlings had significantly greater diameter and height relative growth rates with landscape fabric ($p < 0.05$). The interaction between landscape fabric and gap size was significant for both variables ($p < 0.05$). Tree shelters had a significant positive effect on seedling height (but not diameter) regardless of gap size ($p = 0.001$). Survival was significantly greater in small gaps (73%) compared to large gaps (42%). *Rubus* spp. physically crushed the seedlings and reduced light levels in higher light conditions. In conclusion, we recommend planting chestnut seedlings in small gaps without landscape fabric, or a large gap with herbaceous management. Planted chestnut seedlings compete best under these conditions in an Appalachian cove ecosystem.

Keywords: *Castanea dentata*; *Cryphonectria parasitica*; Height and Diameter; Survival; Southern Appalchain Cove; Gap Size; Tree Shelter; Landscape Fabric

PP96 - Effects of Canopy Gap Size on *Castanea dentata* in the Cumberland Uplands of Tennessee

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Castanea dentata growth and reproduction in the forest ecosystem is limited by the light made available through canopy gaps (Ashe 1911, Paillet 2002). Artificial and existing canopy/light gaps can be used for *C. dentata* seedling establishment for restoration efforts. However, the lack of blight resistant planting material has limited what is known about the silvicultural requirements of *C. dentata*, including establishment in light gaps (Clark et al. 2011). During the 2019 season, we studied the survival and growth of 724 TACF seedlings in 35 various

sized light gaps in the Cumberland Uplands. A hemispherical photograph taken at each seedling allowed calculation of percent canopy openness. We compared canopy openness to the growth rate and survival of the saplings. Two of the study sites were previously planted by the Tennessee Chapter of TACF: the private conservation easement at Eagle Point Railroad (Cumberland Plateau) and the private property of Rogers Starr (Eastern Highland Rim). We established a new site near Barker Pounds trailhead at North Chickamauga Creek Gorge State Natural Area (Cumberland Plateau) with 9 light gaps: 3 small, medium, and large (open field). We measured height, root collar diameter, and survivorship in April/May 2019 and late September/October 2019 (Rhodes et al. 2009). Preliminary results suggest a positive correlation between percent canopy openness and vertical growth over one growing season and a high positive correlation between canopy openness and increase in root crown diameter. At Barker Pounds, first season mortality was 73.1%, but subsequent soil samples tested positive for *Phytophthora cinnamomi* which causes a root rot in *C. dentata*.

PP97 - Biological Monitoring of Oglethorpe Freshwater Wetland, St. Simon's Island, GA.

Taylor Warren, James Deemy, Taylor Martin, Isabelle McCurdy

College of Coastal Georgia, Brunswick, GA

Small, freshwater wetlands on barrier islands are understudied compared to nearby saltmarshes. These wetlands are distinct aquatic ecosystems that appear on southeastern barrier islands. Freshwater wetlands water balances are generally driven by precipitation, soil water flow, and freshwater lens discharge. Barrier island freshwater wetlands serve as small pockets of habitat for salt intolerant (often woody) wetland plants as well as freshwater dependent amphibians, mammals and bird species. The focal wetland for our study is a small semi-isolated wetland on St. Simons Island, GA. Our objectives were to 1) survey canopy and understory vegetation; 2) survey the herpetofauna and avifuana in the wetland; and 3) identify potential indicator species for future biological monitoring. Vegetation was sampled with line intercept transects and point quarter methods during peak growing season (nomenclature follows plants.USDA.gov). Weekly herpetofauna and avifauna surveys were used to determine species richness of these two indicator taxa beginning during late September. Frequent understory plants were lizard's tail (*Saururus cernuus*), common rush (*Juncus effuses*) southern wax myrtle (*Myrica cerifera*), and duckweed (*Lemna* minor). Overstory plants include black gum (*Nyssa sylvatica* var. *biflora*) and red maple (*Acer rubrum*). Herpetofauna species observed in the wetland include: green tree frog (*Hyla cinereal*), bullfrog (*Lithobates catesbeianus*), common brown sink (*Scincella lateralis*). Over twenty avian species were observed including: Prothonotary warbler (*Protonotaria citrea*), tufted titmouse (*Baeolophus bicolor*), blue jay (*Cyanocitta cristata*), Carolina wren (*Thryothorus ludovicianus*) as well as twenty other native bird species. Indicator species identified from our surveys were: duckweed, common green frog and the Prothonotary warbler. More species are expected to appear in the wetland as seasons change and migratory birds pass through the Georgia coast. Additionally, data collected in this study are being used to drive curriculum of the Oglethorpe Elementary School Marsh Lab.

PP98 - Fish farming with food waste: Recycling campus food waste into converted fish flakes (CFF) for zebrafish to explore economical and sustainable aquaculture practices.

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Food is a valuable resource, and its disposal takes up limited space in landfills, where it produces greenhouse gases and toxic leachate. According to NOAA, 2018, about 84% of seafood consumed in the United States is imported, and half of that is sourced from aquaculture. Based on Import Alert 16-124, some farmed fish from China, Canada, and Taiwan were found to be contaminated with environmental toxins, raising food safety concerns (FDA, 2019). One of the reasons the US remains a minor player in the global aquaculture industry is the high cost: commercial fish diets are expensive and contain unsustainably produced fishmeal. To promote economically viable and sustainable domestic fish farming, campus-generated food waste was used to produce "converted fish flakes" (CFF) for a small-scale aquaculture study at Georgia Southern University. After collection from campus dining facilities, food waste was ground and dehydrated. The food waste was analyzed for nutrient composition, and fortification optimized the nutrient profile for zebrafish growth and metabolism. The fortified food waste was converted to CFF and used in this pilot study to feed zebrafish, which have a shorter growth timeline than traditional aquaculture fishes. A total of 100 zebrafish embryos were harvested and grown to juvenile larval stage (~30 days) with a standard lab diet. At the juvenile larval stage, the zebrafish were separated into two groups: Group 1 (n=50) was fed with a standard lab diet and Group 2 (n=50) was fed with CFF. After 75 days, the adult zebrafish were analyzed for weight, health, and reproductive performance. This study demonstrates the feasibility of recycling campus food waste into CFF for zebrafish. Food waste based diets in aquaculture would increase sustainability and profitability, and produce fish that are safer for human consumption than wild caught or traditionally farmed fish.

PP99 - Morphology and genetic analysis of two crayfish species identified in Giles County, Tennessee.

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Crayfish populations are highly imperiled in North America, with threats such as habitat fragmentation, poor water quality, and increased distribution of invasive species. Morphological features used in determining crayfish species continue to be challenging, hence the need for genetic analysis to clarify species identification. The purpose of this study was to survey crayfish size, and perform genetic analysis to determine crayfish species at three creeks in southern Tennessee. Hand-held seines were used to collect crayfish and measurements determined gender, carapace length (CL-mm), total length (TL-mm), and weight (g). An E.Z.N.A. tissue kit was used to extract DNA, followed by polymerase chain reaction (PCR) analysis and sequencing. Crayfish FL differed significantly among sites (ANOVA, $F(2, 81) = 5.671$; $p < 0.05$). Weight and CL did not differ significantly among sites ($p > 0.05$) respectively. Genetic analysis and sequences identified *Orconectes wright* and *Faxonius durelli* as the main species in this region. This is the first identification of these species within this region, and continued research will determine species distribution

PP100 - Conversion of Waste Biomass from Algal Turf Scrubber(ATS)™ Technology into Ceramic Products for Sustainable Use

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Eutrophication is a type of water pollution in which nutrient inputs can cause excessive algal growth which depletes oxygen levels in both marine and freshwater environments. Algal turf scrubber (ATS)™ technology is a potential solution to this problem. Georgia Southern University has been operating an experimental 12 lane ATS unit in Savannah, Georgia. Water is pumped from the Wilmington River and channeled through ATS raceways where algal communities quickly establish and grow. Pumped water flows over the algae allowing them to uptake the nutrients before being returned to the river. When the algae are harvested each week, the biomass itself can become a waste product with a high (~ 30 ppt) salt content. Currently most waste-products from this ATS system are being sent to landfills. Our initial goal was to determine if we could identify insects that might degrade the waste products; however, the high salinity made it inhabitable to most detritivores. During our preliminary studies, we made the observation that as the algal biomass dehydrates, it forms a hard clay-like brick. To determine if the material could be turned into a ceramic product, we dried the algal biomass, pulverized it, and then rehydrated it to form malleable clay that we shaped into disks. These disks were then fired in a kiln. For half of the samples, the algae was rinsed using a centrifuge to reduce the salinity of the clay product to ~4 ppt. Our results show that the algal waste biomass can be used to create ceramic products that are sturdy and have a very high potential for a sustainable, utilitarian or ornamental use.

PP101 - Detection of microplastics in the fecal matter of juvenile sea turtles in Roatan, Honduras

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Microplastics are an ever-growing issue for marine habitats. Many marine species have been found to ingest them, and the full scope of their physiological impact is not well understood. In this study, fecal analysis will be performed to determine if sea turtles, primarily Hawksbills (*Eretmochelys imbricate*), from the marine reserve of Roatan, Honduras have ingested microplastics. The fecal examples (n=5) will undergo a series of separation stages and Nile Red treatment to use microscopy detection via fluorescence. Additionally, sponge (*Geodia neptuni*) samples (n=31) were collected for future research regarding the diet and microplastic ingestion of Hawksbill sea turtles. It is expected that few microplastics will be found in the samples due to consistent efforts of the community to reduce marine plastic pollution. However, plastic pollution is not as well controlled in the terrestrial habitat and may contribute to the presence of microplastics if found.

PP102 - Algae Biomass Removed from Algal Turf Scrubbers as a Nutrient Source in the Nursery Production of *Spartina alterniflora*

Tessa Murrell, Heather Joesting

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Spartina alterniflora is the dominant salt marsh plant along the East Coast of the US and plays a key role in marsh growth and maintenance. Thus, this species is often planted as part of coastal salt marsh restoration projects. Nursery production of *S. alterniflora* requires frequent fertilization, often using commercial fertilizers, and can represent a significant cost to nurseries. Algae removed from algal turf scrubbers (ATS), which are designed to remove nutrients from a water body through incorporation into algal biomass, may serve as a natural alternative to commercial fertilizers and provide the critical nutrients required for *S. alterniflora* growth. The aim of this research was to determine if algae removed from an ATS can be used as a nutrient source in the nursery production of S. *alterniflora. S. alterniflora* plugs were planted in three different treatments and cut back for winter senescence: (1) Control (no nutrient source), (2) Osmocote (commercial fertilizer), and (3) dried algae removed from ATS. Regrowth (e.g., weekly plant height and number of ramets) will be monitored beginning in January, and plant growth and biomass will be compared among treatments to determine the fertilizer potential of algae removed from an ATS. Use of this algae as a nutrient source in the nursery production of *S. alterniflora* would not only provide a more cost effective and natural nutrient source for nursery production of *S. alterniflora* but may also improve restoration success by providing nutrient sources similar to salt marsh environments.

PP103 - Collaboration with local crabbers: utilizing blue crab morphometric analysis to inform bycatch reduction solutions for the Diamondback Terrapin

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Diamondback terrapins (*Malaclemys terrapin*) are considered Vulnerable by the IUCN Red List and face a wide variety of ecological and anthropogenic threats. One of the largest threats to terrapins is accidental drowning in commercial fishing gear and blue crab (*Callinectes sapidus*) pots. Bycatch Reduction Devices (BRDs) may drastically decrease terrapin mortality rates associated with drowning in commercial fishing pots but are not currently mandated in the state of North Carolina. The North Carolina Blue Crab Fishery is listed as a fishery to avoid by the Monterey Bay Aquarium Seafood Watch, due in part to the lack of measures to prevent terrapin bycatch. This designation could yield a negative economic impact on the crabbers in addition to the negative ecological impact of accidental bycatch.

The goal of this project is to determine the typical size range of the legal-sized crab catch in Eastern North Carolina. Crab morphometric data were collected by measuring crabs harvested by local crabbers from coastal estuarine (Masonboro Island) and river (Cape Fear) systems. Data will be analyzed to assess spatial and temporal patterns in crab size and compared to historic data from 1997-2019 provided by the North Carolina Department of Marine Fisheries (NC DMF).

Preliminary analyses show that in the Cape Fear River, carapace medial length, maximum length, and maximum height averaged at 65.05 mm, 67.65 mm, and 34.95 while crabs from Masonboro Island averaged 68.12 mm, 70.03 mm, and 37.50 mm, respectively. These data will provide insight as to how BRD implementation may affect crab catch within different habitats. Our study will contribute to efforts addressing the issue of fisheries bycatch by proposing science-based solutions that have the greatest ecological benefit without imposing economic harm on the local crabbers. Future research will be performed to test the proposed devices to determine efficacy.

PP104 - The Effects of the Golden Ray Capsizing on Georgia's Marsh Vegetation

Hollie Hancock, James Deemy, Kimberly Takagi

College of Coastal Georgia, Brunswick, GA

The Effects of the Golden Ray Capsizing on Georgia's Marsh Vegetation

Hollie L. Hancock, Kimberly K. Takagi, James B. Deemy

The College of Coastal Georgia, Brunswick GA (USA)

On September 8, 2019, the *Golden Ray*, a 200 m long transport vessel with 4,200 cars onboard, ran aground in Saint Simon's Sound and capsized. Since that time, oil and gas have been leaking into the surrounding waters and marsh. Salt marshes provide many ecosystem services such as storm buffering, pollutant filtration and nursery habitat for commercially important fish and shellfish stocks. Our objective of this study was to evaluate the effects of oil and gas from the *Golden Ray* on marsh vegetation. Three marsh sites on Saint Simons Island and three marsh sites on Jekyll Island were selected as focal sampling locations. Vegetation cover was measured using 100 m line transect methods at each sampling location. Our preliminary data indicate positive relationship between distance from the *Golden Ray* and all vegetation cover. This study provides baseline vegetation data for measuring the potential impacts of the *Golden Ray* on local salt marsh vegetation. Further research is needed to determine whether the die off is due to the effects of shipping oil or the changing seasons. This study also serves as the beginning of a long-term monitoring project that will assess marsh recovery over time.

PP105 - Beaten black and blue: assessing the role of melanization in territorial encounters of the eastern fence lizard

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Colorful visual signals are often used across animal species to convey information during aggressive male-male encounters. The information content of these color signals has received much study, but how receivers interpret this information has received less attention. Most male lizards in the genus *Sceloporus* have paired blue belly patches rimmed with black borders that are actively displayed during territorial disputes. Previous work has examined how receivers interpret the size of the blue belly patches, but it is unclear whether the black borders convey information that is assessed. Here, using territorial male *Sceloporus undulatus* lizards in the field, we examined receiver response to intruders with different sized black borders (manipulated with paint) to determine (a) if melanization conveys information assessed during aggressive encounters, and (b) how receivers respond to these putative signals. We found that when presented with intruders with small black borders, free-ranging males had higher frequencies of attacks. There were no differences in information-gathering behaviors (headbobs and latency to respond) when free-ranging males were presented with intruders with large and small black borders. This indicates that the black borders do convey meaningful information assessed during aggressive encounters, and the transfer of this information is immediate. Receivers are able to extract information from these black signals very quickly, without needing to further assess the signal through information-gathering behaviors.

PP106 - Three's a crowd: population differences in behavior among three species of the *Sceloporus undulatus* complex

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Animals communicate in complex environments, with a suite of different factors that can shape signal design. Some animals live in more dense, closed environments, whereas others live in more open, exposed environments. Lizards in the genus, *Sceloporus*, have a complex signaling system for communicating with conspecifics. They use motion in the form of species typical headbob patterns, chemical signaling in the form of femoral pore secretions, and color signals in the form of blue belly patches. Here, we examine signal use across three closely related populations of *Sceloporus* lizards from diverse habitats across the United States, to explore the role of habitat in shaping communicative signals. We filmed baseline levels of activity for free-ranging males of three populations of the *Sceloporus undulatus* complex: *S. undulatus hyacinthinus* (found along an artificial lake near a deciduous forest in Indiana), *S. consobrinus* (found on boulders between mixed-grass prairie and mesic oak shrubland in Colorado), and *S. undulatus undulatus* (found in an upland pine forest in Georgia). Then, we scored frequency and rates of behaviors important for communication. These included chemosensing behaviors (e.g. tongue-flicks, nose taps, chin wipes, lip smacks) and visual display behaviors (e.g. headbobs). We found that populations differed in their use of communicative signals, perhaps as an adaptation to environmental features. *Sceloporus undulatus hyacinthinus* had particularly low levels of chemosensing behaviors, whereas *S. consobrinus* had the highest levels of headbob displays. All three populations had positive correlations between headbobs and chemosensing behavioral use, supporting the redundant signal hypothesis. This study adds to the growing body of evidence that habitat can have profound impacts on signal use, even among closely related populations.

PP107 - The Response of Rodents to Native and Non-Native Predator Scent Cues

Paloma Avila, Lindsey Ansley, Sean Beckmann, Terence Farrell

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Predatory avoidance is key to survival for small mammals. As such, the ability to identify potential predators is a selective advantage. Rodents are primarily olfactory species that commonly are prey for other organisms, including snakes. Based on this, we would expect that rodents would use scent cues to identify and avoid predators. However, few studies have explored the effect of snake scent cues on rodent avoidance behavior. We hypothesized that rodents will avoid scents of potential serpent predators. Additionally, rodents are more likely to avoid the scents of native predators than non-native predators. To test this, Sherman traps were placed in a randomized block design in a forested area. Traps were organized into blocks of four containing newspaper with one of four randomly assigned scents; reticulated python, eastern diamondback rattle, yellow rat snake, and a non-scented control. Traps were checked daily and captured rodents were identified to species and marked to avoid pseudoreplication. Trapping rates for the different odor cues were compared using chi square goodness of fit tests. Three species of rodents were captured as part of this study. Our results show that scent type had no impact on *Peromyscus* mice. Hispid cotton rats, *Sigmodon hispidus*, were more likely to be found in control traps suggestion avoidance of all predator scents. Woodrats, *Neotoma floridana,* were significantly more likely to be found in python-scented traps than any others. This suggests either an increased likelihood to explore novel scents (non-native snakes) or that woodrats are actually attracted to the scent of pythons. While further research is needed to identify the cause of increased woodrat activity, these results have important conservation implications for areas where woodrats and pythons coexist.

PP108 - Analyzing the effects of urbanization on the instance of mimicry in gray catbird (Dumetella carolinensis) song

Christopher Will, Dana Moseley

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Urbanization and anthropogenic noise have direct impacts on species habitats and behavior. One species especially impacted by noise pollution are those that communicate acoustically, such as birds using songs as mating signals. The gray catbird, (*Dumetella carolinensis*), is a vocal mimic belonging to the Mimidae family, and is found across various levels of urbanization. We hypothesize that urbanization impacts the ecological and acoustic community and thus will affect the mimicry in catbirds' songs. Songs were recorded across urban gradients in Virginia and Washington D.C. We analyzed recordings in Raven sound analysis software and identified mimicry of nine indicator species representing urban to rural birds. We predicted that the immediate bird community diversity will impact the incidence of mimicry in catbird song repertoires. Additionally, we predicted that the more species of birds within a territory, the larger repertoire of mimicry males will have. Results support our hypothesis that urban gradients impact the immediate diversity of species present. Catbirds breeding in urban habitats sang mimicry of more urban species such as starlings and robins, while catbirds in more rural habitats mimicked more rare species in their songs. Understanding how urbanization impacts species' mating signals and potentially mating success, for urban-adapting species such as the gray catbird, will contribute to conservation efforts and future studies on species that persist in urbanized landscapes.

PP109 - The Nonindigenous Asian clam, *Corbicula fluminea,* in New Hampshire

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The nonindigenous Asian clam, *Corbicula fluminea*, continues to spread northward into cooler waters of the northeast. This range extension has been attributed to thermal discharges acting as thermal refugia. We conducted an extensive survey for *C. fluminea* in New Hampshire waters lacking artificial thermal influence. Using scuba, divers searched for evidence of *C. fluminea* at 67 south-central and southeastern New Hampshire locations. We found 6 new locations with Asian clams for a total of 11 sites in New Hampshire without thermal discharge. Sites with Asian clams were limited to south-central and southeastern New Hampshire. Continued expansion of Asian clam into northern cold waters suggests that thermal refugia are not necessary and that the Asian clam populations may contain genetic variability and/or adaptations to withstand cold winter water temperatures.

PP110 - Feeding Behavior of the Aquatic Snail (*Physella acuta*) After Exposure to Different Levels of Ammonium Phosphate

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Although commercial fertilizer is widely used to increase plant production, there is concern that components of fertilizer during runoff have a negative effect on aquatic life. Previous studies have shown that chemicals commonly found in fertilizer such as cadmium, nitrogen, and aluminum, negatively affect aquatic organisms such as *Physella acuta,* an ordinary pond snail. Overall wellbeing of aquatic organisms is frequently measured by observing feeding behavior. In fact, feeding behavior has been used in several studies to demonstrate negative consequences in snails. Although several compounds found in fertilizer have been shown to detrimentally affect the feeding behavior of *P. acuta*, the effect of a common ingredient, ammonium phosphate, on snail feeding behavior has not been studied. The purpose of this study was to examine the feeding behavior of snails exposed to several concentrations of aqueous ammonium phosphate. Preliminary results suggest that low levels of ammonium phosphate did not significantly affect feeding behavior in *P. acuta*.

PP111 - Comparing Water Quality for Aquaponics Systems with Different Solids Removal Methods, Biofilter Media, and Effluent Output to Grow Beds

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Aquaponics is a sustainable food production method that combines fish production via traditional aquaculture and crop growth through hydroponics in a closed-loop, recirculating system. Food production through aquaponics uses 95% less water than traditional aquaculture and agriculture and has the potential to provide fresh, nutritious food to areas with food insecurity. However, challenges remain in the development of a sustainable aquaponics industry, primarily due to the high operating costs (e.g., electricity demand, fish feed procurement). To overcome these challenges, technologies must be developed to reduce operating costs and/or increase crop/fish production. The goal of this study was to compare water quality between two aquaponics systems that differ in basic design elements: System 1 used a sock filter for solid removal and Kaldnes media for the biofilter and had multiple effluent inputs to the hydroponic grow bed while System 2 used a backwash settling chamber for solids removal and biobeads as biofilter media and had a single effluent input into grow bed. In each system, nitrate, ammonium, potassium, pH, dissolved oxygen, and conductivity (indicative of total suspended solids) were measured weekly at various locations from August to December 2019. Results showed significantly less ammonium, nitrate, potassium, and conductivity and significantly greater dissolved oxygen in System 1 compared to System 2. Furthermore, there was complete removal of ammonium in System 1 prior to circulation back into fish production while ammonium was decreased by ~57% in System 2. These results suggest that the design of System 1 results in more optimal conditions for fish and plant production. Determining optimal aquaponics designs that maximize fish and plant production will be critical in the development of a strong and competitive aquaponics industry.

PP112 - Comparing basil production in two aquaponics systems with different solid removal methods, biofilter media, and grow bed effluent output

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Aquaponics is a form of crop and fish production that combines conventional aquaculture and hydroponics to create a closed-loop, recirculating growth system that uses 95% less water than traditional aquaculture and agriculture practices. However, some challenges remain in the development of a sustainable and profitable aquaponics industry, primarily due to the energy demand for system operation. To overcome these challenges, technologies that reduce energy input and/or increase crop/fish production must be developed. The aim of this research was to compare basil production in hydroponic grow beds for two aquaponics systems that differ in the method of solid removal (backwash settling chamber vs. sock filter), biofilter media (biobeads vs. Kaldnes media), and effluent input into the grow bed (single input vs. multiple inputs). Specifically, basil growth and productivity were measured in three separate locations within the grow beds of both system designs over an 8 week period. Results showed significantly greater final plant height, mean weekly growth rate, aboveground and belowground biomass, and total biomass in the system using sock filtration, Kaldnes media, and multiple effluent inputs into plant grow beds. Furthermore, there was no significant difference in final plant height and mean weekly growth rate in the three locations within the grow beds for this system design, suggesting that nutrients were efficiently circulated within the grow bed. Overall, the results suggest that an aquaponic system using sock filtration, Kaldnes media, and multiple effluent outlets into grow beds efficiently circulates nutrients, resulting in increased basil growth and productivity. The increased plant production resulting from this aquaponic system design has the potential to contribute to increasing the viability, productivity, and profitability of the aquaponics industry.

PP113 - Exploring the Compounding Effects of Common Herbicides on Freshwater Microbiomes

Gabriel Hooper, Nathan Edmondson, John Hoverson, Mark Fischer, Kyle J. Harris, Matthew Becker

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The prevalent use of pesticides throughout the United States has resulted in unintended negative consequences for non-target organisms. Run-off can move multiple pesticides into environments bringing them into contact with non-target organisms that have variable tolerances to pollution. There are limited studies on how the compounding effects of pollutants impact freshwater microbial assemblages. Previous research conducted by our lab observed that acute treatment of common herbicides on crayfish annelid ectosymbionts resulted in mortality. Therefore, we selected a similar combined treatment to investigate the effect of these environmentally relevant pesticide concentrations on the microbial assemblages of the crayfish and their environment (sediment and water).

This project examines these microbial community assemblages (MCA) before and after a 48-hour exposure to 2000 ppb of herbicides (glyphosate, atrazine, and 2,4-D). DNA was extracted and the 16S gene was amplified using PCR. These samples will be sequenced and then analyzed using the bioinformatics software QIIME2. This project seeks to answer two questions: 1) Will acute exposure to pesticides reduce bacterial diversity and richness within a freshwater environment (water and substrate) and on biota (crayfish)? and 2) Will the exposed MCA reveal that some bacterial populations are more resilient under acute pesticide exposure? We expect that acute pesticide exposure will: 1) reduce bacterial diversity and richness across sample types and 2) that the acute exposure will result in a shift in bacterial populations which predominate in the resulting MCA's. This study seeks to improve our understanding of how an acute exposure to pesticides may restructure microbial communities on crayfish hosts and freshwater environments.

PP114 - Habitat Heterogeneity and Fish Communities Relative to Debris Dams in East Fork Indian Creek, Menifee County, KY

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Large woody debris influences many physical and biological aspects of stream ecosystems. One way woody debris can be arranged in a stream is as a debris dam. While studies have shown that debris dams can retain large amounts of particulate matter and support more abundant and diverse invertebrate communities, few studies have assessed their influence on fish. In this study we assessed how woody debris dams alter habitat heterogeneity, fish diversity, fish biomass, and fish communities upstream and downstream of dams in East Fork Indian Creek at the Red River Gorge in Menifee County, KY. Overall, debris dams did not significantly alter any response variable ($p>0.05$). This may likely be because East Fork Indian Creek is a high gradient stream with large boulder substrate. Previous studies have found that the influences of large woody debris are largely hindered in these types of environments because large boulders already provide habitat heterogeneity for diverse communities. These results suggest that debris dams may act in a similar manner. The findings of this study can aid ongoing restoration efforts at East Fork Indian Creek.

PP115 - Effects of sediment on the foraging success of Subarctic sticklebacks: A preliminary study

Seth Drake, Jon Davenport

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Little is known about factors influencing the feeding ecology of Stickleback fish (*Pungitius pungitius*, Ninespine stickleback; *Culaea inconstans*, Brook stickleback) within Subarctic wetland ecosystems. Habitat complexity has been hypothesized as one of the major influences on foraging success of fish. Therefore, we evaluated the effects of habitat complexity (either organic or sand sediment) on the feeding ecology of both species of sticklebacks. We conducted a short-term mesocosm experiment with both pelagic (copepods) and benthic (midge larvae) prey during September 2019. Based on field data, we hypothesized that Ninespine sticklebacks would have greater foraging success on both open water and benthic based prey relative to Brook sticklebacks, regardless of habitat complexity. We also hypothesized that benthic prey would have higher survival compared to pelagic prey with both fish species and this would be enhanced by organic sediments. Our experiments ran for 24 hours using 37.8 L tanks in which sediment type (either organic or sand sediment) was crossed with fish presence (Ninepspine alone, Brook alone, or no fish predator). Midge larvae abundance was significantly affected by fish presence, but the strength of fish presence was reduced with the presence of organic sediment. Copepod and total prey abundance was only negatively affected by fish presence with no difference between the two stickleback species. It also appears that only the benthic prey species may benefit from different pond sediment types. Overall, our results indicate that both stickleback species can be voracious predators on aquatic invertebrates.

PP116 - The effects of detritivores on leaf litter breakdown in experimental ponds

Logan Suchniak, Ali Montazeri, Robert Creed, Jon Davenport

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Caddisfly larvae and crayfish can play a major role in stream food webs by having strong negative effects on leaf litter breakdown. However, less is known about their role in pond food webs and subsequent impacts on ecosystem function. To evaluate the effects of two common species inhabiting ponds in the NC mountains (the caddisfly *Platycentropus* spp. and the crayfish, *Cambarus bartonii*), we conducted a mesocosm experiment. We deployed four different food webs (1 large crayfish, 2 small crayfish, 11-15 caddisflies, or no detritivores) to determine the effects of these detritivores on a common leaf litter type (Oak) over 6 weeks. To standardize detritivore biomass, treatments had different densities. We found a marginally significant effect of detritivore treatment on leaf litter decomposition relative to leaf litter controls. Leaf litter biomass did decline through time but was dependent on detritivore identity. Specifically, the effects of two small crayfish caused the greatest decline by the conclusion of the experiment. Our results indicate that detritivores can have effects on pond leaf litter but that this effect may be limited based on species and body size. Future studies should expand and explore the greater range of conditions (detritivore densities, top predator presence, resource availability) that could explain the role of caddisflies and crayfish in pond food webs.

PP117 - Effectiveness of Stream Restoration on Benthic Macroinvertebrate Communities and Water Quality

David Wilcox, Rhett Elliott, Brittany Sweet, Haley Grove, Lauren Charles, Kathryn Motley, Luke Shiley, Camden Brewer, William Hunter, Bruce Wiggins

James Madison University, Harrisonburg, VA

The Shenandoah Valley encompasses some of the highest agricultural producing regions in Virginia, many of which are large contributors of nutrients and sediment to receiving waterways. To help reduce this pollution, the Conservation Reserve Enhancement Program (CREP) assists landowners in the installation of riparian restoration projects in which cattle are fenced out or a riparian buffer is planted. We examined the temporal effects of riparian restoration and the impact of upstream landuse on water quality for eleven farms participating in the CREP program for various times (from 1 to 14 years). We hypothesized that the length of time that the CREP program has been established would have a positive effect on the water quality of a stream. Water quality was quantified by measuring benthic macroinvertebrate assemblages using the Hilsenhoff Biotic Index (HBI), Virginia Stream Condition Index (VA-SCI), and the Shannon Diversity Index. GIS analysis was also employed to calculate upstream land use and stream channel characteristics: land use, canopy cover, slope, impervious surface, relief, road density, and watershed area were assessed for the watersheds and 100-meter stream buffers at each sampling site. Single variable and multiple linear regressions were performed separately within the watershed and buffer zones. The time

since restoration showed a significant positive relationship with VA-SCI ($R^2 = 0.441$, $p = 0.007$) and a significant negative relationship with HBI ($R^2 = 0.267$, $p = 0.049$). When upstream landuse variables were included in multiple regressions, the relationships were stronger: time since restoration, the percentage of upstream agricultural land use and impervious surfaces predicted VA-SCI values (adj $R^2 = 0.579$, $p = 0.005$) and HBI values (adj $R^2 = 0.452$, $p = 0.011$). These data show that CREP efforts are having a positive effect on water quality, and that upstream land use is also an important factor.

PP118 - Exploring the Sub-Lethal Effects of Pesticide Pollution in Crayfish

Brittany Carnathan[1], Zachary Youngbar[2], Megan Pizzo[2], Kathryn StClair[2], Kyle J. Harris[2]

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Freshwater systems bordering agricultural practices can be prone to having pollutants (e.g. pesticides) introduced via runoff during rainfall events. These pollutants can have damaging effects on the living organisms throughout these systems. Nationwide agricultural industry puts local freshwater ecosystems at potential risk for the unintentional introduction of pesticides. Low doses of pesticides (e.g. three commonly used pesticides being Atrazine (ATZ), Glyphosate (GLY), and 2, 4-D) have been shown to negatively affect non-target organisms (e.g. macroinvertebrates). Research has indicated that these pesticides can have detrimental effects on non-target organisms by compromising their metabolic function and overall health. This project aims to expand the existing knowledge of how pesticide introduction to freshwater environments affects a common non-target organism (crayfish) by looking for sub-lethal effects from acute and chronic exposure.

Crayfish from a forested stream with limited exposure to anthropogenic impacts were exposed to an acute 48-hour burst and a chronic exposure (multiple weeks) of ATZ, GLY, and 2, 4-D at 500ppb and 50ppb respectively. After exposure, the sub-lethal effects of the pesticides on the crayfish were assessed for tissue degradation of the hepatopancreas, a primary site of detoxification in crayfish. The apical end of the hepatopancreas was removed from each crayfish. The tissue was blocked, and cross sections were made using a cryostat. The slides were then stained with DAPI to fluoresce individual cells and counted using an EVOS M5000 imaging system. Preliminary analysis on cell counts reveals a significant degradation of tissue when exposed to these common pesticides. This study reveals how environmentally relevant combinations of pesticides can have sub-lethal impacts on non-target freshwater organisms.

PP119 - Surveillance of microplastic pollution in Central Virginia freshwater ecosystems

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Microplastic pollution of water sources and subsequent impacts on aquatic organisms is an emerging topic in the scientific community. Aquatic organisms often mistake microplastic particulates (MP) as food and inadvertently ingest the particulates, which can biomagnify through the food chain. While the frequency of MP ingestion is well-researched in the marine environment, little is known about the prevalence and consequent impacts of microplastics on freshwater organisms. This research project explores the occurrence of microplastic pollution on an abundant and ecologically important freshwater invertebrate species: crayfish. Crayfish from two Central Virginia streams are collected to: (1) identify MP in the digestive tracts and gill filaments of crayfish; (2) quantify the MP using analytical chemistry techniques; (3) characterize the MP using a plastic library developed from clippings of Rock Castle plastic pollution; and (4) consider the physiological and ecological implications of MP contamination of crayfish species and potential public health risks.

Preliminary investigations have confirmed the identity of a polypropylene fiber in the digestive tract of an urban crayfish. Moreover, recent examinations of gill filaments in additional organisms have revealed colorful foreign fibers embedded in the gill tissues. Upon further research, it is expected that: (1) additional MP will be identified in the digestive tracts and gill filaments of crayfish collected from both study sites; (2) the techniques to isolate MP from tissue samples will result in more MP being identified; and (3) the occurrence of MP in the urban stream will be greater than that of the rural stream due to its location near commercial businesses and the dominant thoroughfare. The substantiated results from the preliminary investigations provide compelling evidence for microplastic contaminants in the digestive tracts and gill filaments of crayfish. Therefore, the discovery of these fibers demonstrates that crayfish are consuming plastic pollution in Central Virginia streams.

PP120 - Preliminary estimates of Estrogen levels in local waterways using ELISA with ImageJ ReadPlate plugin analysis

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Synthetic Estrogen (EE2) is often found in waterway environments due to human waste or pharmaceutical disposal. An ELISA detection kit was purchased for detection of EE2 in the environment. ImageJ contains multiple plugins for processing and analyses. The particular plugin for this test is called ReadPlate. ReadPlate measures the absorbance of an image of a multi-well plate up to 96 wells. ImageJ ReadPlate was used to read 96-well plates. This test is intended to detect how much EE2 is in waterways of Northeast Alabama. The water tested was from Germania Springs, Lake Heflin, Hane's Branch Creek, Cane Creek, and Weaver's Creek. A 100 mL bottle of water was collected above and below the water treatment plants at each location. Germania Springs is a natural underground spring and is being used as the control. To test the accuracy of the ImageJ Plugin for absorbances, comparisons with a spectrophotometer were made using methylene blue and a Bradford protein analysis kit. The plate was placed in a light box and a picture of the plate was taken and analyzed on ImageJ. The data from ImageJ using the red channel was more consistent with the absorbances from the spectrophotometer than the other channels on ImageJ.

PP121 - Ecotoxicological Effects of 4-Methylcyclohexanemethanol on General Esterase and Glutathione S-Transferase Activity in Fathead Minnows, Pimephales promelas.

Emily De Wind, Benjamin Thornton

Southern Adventist University, Collegedale, TN

In 2014, several thousand gallons of coal-processing chemicals, including 4-methyl-1- cyclohexanemethanol (MCHM), spilled into the Elk River in West Virginia. Although some initial studies did consider the effects of MCHM exposure on humans, little attention has been given to the aquatic biota. In this project, fathead minnows, *Pimephales promelas*, an environmentally relevant model organism, were exposed to 0 ppm, 5 ppm, 10 ppm, 20 ppm, and 50 ppm of MCHM for 72 hours. Whole body protein extraction was used to measure specific activity of two detoxification enzymes, general esterase and glutathione-*s*-transferase. General esterase activity was determined by monitoring the hydrolysis of para-nitrophenyl acetate at 405 nm for 60 readings (5 s intervals) and using a molar extinction coefficient of 6.53mM^{-1}/mM/cm and corrected path length of 0.6135 cm. Glutathione-*s*-transferase activity was determined by monitoring the hydrolysis of 1-chloro-2, 4-dinitrobenzene at 340 nm for 30 readings (no interval) and a mole extinction coefficient of 9.6 /mM/cm and corrected path length of 0.5756 cm.

We expect to see a significant difference in enzyme activity between the experimental groups and the controls. If enzyme activity is dys-regulated due to exposure to MCHM, it is possible that the same exposure could impact endogenous functions of these enzyme systems, thus leading to more specific inquiries regarding the affects of MCHM in aquatic biota.

PP122 - Water Quality and Bacterial Abundance of Urban and Rural Streams at Similar Elevations in the South Carolina Piedmont

Justin Chang, Greg Lewis, Brannon Andersen

Furman University, Greenville, SC

Urban environments can negatively affect stream water quality. For example, urban streams may receive inputs of nutrients and bacteria from impervious surfaces, lawns, and leaking sewer lines. Previous studies in the South Carolina Piedmont, a region experiencing rapid urban development, have shown that solute and bacteria concentrations in forested headwater streams can vary naturally with elevation. Consequently, elevation could act as a confounding variable when comparing urban and rural streams. We examined water quality and bacterial abundance differences between urban and rural streams of similar elevation in the South Carolina Piedmont region. During June-July 2019, dissolved nutrients and abundance of suspended bacteria were measured in 12 urban streams and 7 rural streams draining watersheds of 1.2 to 9.4 km^2. For both urban and rural streams, elevation of sampling sites ranged from 246 to 292 meters. Land cover in the watersheds of urban streams was 15-44% impervious and < 22% forested. By contrast, land cover in the watersheds of rural streams was <1% impervious and 21-90% forested. Water temperature, pH, dissolved oxygen, and specific conductance were measured at each site. Water samples were analyzed in the laboratory for solute concentrations and bacterial abundances. Temperature, specific conductance, and concentrations of *Escherichia coli*, total heterotrophic bacteria, sodium, calcium, chloride, sulfate, nitrate, total dissolved nitrogen, and dissolved organic carbon, were significantly higher in urban streams than rural streams. However, we found no significant differences in pH, dissolved oxygen, turbidity, or concentrations of total coliforms, enterococci, bicarbonate, magnesium, dissolved silicon, dissolved iron, ammonium, or dissolved organic nitrogen between urban and rural streams. The differences in water quality between urban and rural streams we have documented are consistent with results of studies from other regions.

PP123 - Quantification of Microplastics in the Catawba River Basin

Chasity Moore, Cynthia Tant

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Plastic pollution has become a worldwide ecological and economic issue. An overproduction of plastic and improper disposal have caused plastic to be ubiquitous in the environment. Plastic, and more recently microplastic (plastic pieces smaller than 5mm), pollution in the aquatic ecosystems has become a major area of concern due to the occurrence of plastic in the guts of many aquatic species. Most research has focused on marine microplastics; however, there has been very little research on inland freshwaters. In this study we focused on the Catawba River and its tributaries in South Carolina to quantify microplastics in surface water, sediment, and invasive freshwater bivalves, *Corbicula fluminea*. Samples were processed and quantified using the NightSea© fluorescent microscope adaptor. We found that tributaries had significant differences in the quantity of microplastics for surface water, sediment, and bivalves, and storm flows increased the quantity of microplastics in surface water samples. These data fill previous knowledge gaps in freshwater microplastic research in one of South Carolina's major river basins.

PP124 - Prevalence of Microplastic Debris and Ingestion in Fishes and Bivalves from Lake Sidney Lanier, Georgia

Hannah Dell, Mattias Johansson, Grace Roa

University of North Georgia - Gainesville, Oakwood, GA

Microplastics are a new pollutant that have grown of increasing concern over the past years. These pollutants can be described as small particles, fragments, or fibers of plastic measuring less than 5 mm in length. Microplastics can be found in both marine and freshwater environments, creating concern for the aquatic organisms which can be directly impacted through ingestion of such particles. While most of the research conducted regarding microplastics involves marine environments, research involving freshwater environments has become increasingly imperative. To address this research gap, we are exploring the impacts on freshwater organisms found in Lake Sidney Lanier located in Gainesville, Georgia. Initial investigation consisted of visual surveys of the water column using plankton tows at multiple

sites on the lake. Further investigation will look at the ingestion of microplastic within small fishes and the invasive Asian Clam (*Corbicula fluminea*). While some microplastics were visually found upon analysis of water samples, further confirmation of specific plastics was attained using mass spectrometry. If organisms in the lake are ingesting these microplastics, impacts could include bioaccumulation of toxins in the food chain or decreased feeding, potentially leading to decreased growth of individuals or population declines.

PP125 - Decadal leaf-fall input to a deciduous woodland headwater stream

Clay Runck

Georgia Gwinnett College, Lawrenceville, GA

First-order headwater streams are the most common aquatic environment of landscapes, and as such they are important sites for organic matter processing, nutrient cycling, and biodiversity. These small streams are not isolated from the terrestrial environments through which they flow. Seasonal input of leaf fall from riparian vegetation comprises the bulk of the energy base for secondary production in small headwater streams in deciduous forests. Thus, the productivity of these systems is highly dependent on energy and nutrients contained in organic matter derived from terrestrial primary production. Headwater streams are not just receivers of energy subsidies, they also provide subsidies of energy and nutrients to riparian and terrestrial environments. Examples of cross-ecosystem subsidies from headwater streams to terrestrial food webs include emergence production of adult aquatic insects and biomass of crayfish, amphibians, and fish consumed by aquatic-terrestrial wading consumers such as raccoons and herons. This study reports 10 years of leaf-fall input to a first-order headwater stream in a deciduous forest watershed on the campus of Georgia Gwinnett College. Annual leaf-fall biomass input to the stream averaged 396 grams dry-mass/m^2 (g DM; 1 standard deviation = 98 g DM/m^2). There were significant differences in annual leaf-fall biomass over the 10 years of measurement ($p < 0.001$). Annual means varied by a factor of 2.4, from a low of 222 g DM ($\pm$ 8 g DM/m^2; 2011) to 538 g DM ($\pm$ 50 g DM/m^2; 2009). However, no significant relationships ($p > 0.05$) were detected between leaf-fall input and climate variables (e.g., precipitation, temperature, degree days, growing days, etc.; soil moisture and depth to water table were not measured in this study). Leaf production by mature, well-established trees in the vicinity of this groundwater fed stream are likely not limited by availability of water even during drought years.

PP126 - Microhabitat type use by benthic macroinvertebrates in the Lee Branch stream on the Midway University Campus: a preliminary look

John Delfino, Guipsy Lopez

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The Lee Branch stream flows on the Midway University Campus with its two reaches surrounded by natural terrestrial habitat. We studied the ecology of these reaches in summer 2016, and reported findings in 2017 for biological condition, water quality at benthic macroinvertebrate sites, and associations between benthic macroinvertebrate group and habitat type. With that summer 2016 data, we reported findings in 2019 for structural (habitat types and microhabitat combination types) and biological (benthic macroinvertebrate groups) diversity and evenness in these two reaches. Here in 2020, with this summer 2016 data in hand, we report on association between benthic macroinvertebrate group and microhabitat combination type in each habitat type found in each stream reach. For each reach we identified and quantified habitat types as riffles, runs, pools, and glides, and generally randomly sampled each for benthic macroinvertebrates. We collected benthic macroinvertebrates using a D-frame net. In the lab we identified and preserved them; crayfish were released. Within habitat type we identified and quantified microhabitat combination types within 1-m^2 quadrats. Stream reach 1 (≈237 m) supported the following sampled totals: 4 riffles (9 substantial contributors to an association, 3234 benthic macroinvertebrates, 21 benthic macroinvertebrate groups, 7 microhabitat combination types, 5 benthic macroinvertebrate groups with numbers of individuals greater than expected in microhabitat combination type); 4 runs (2, 1602, 11, 3, 1). Stream reach 2 (≈1338 m) supported these sampled totals: 10 riffles (19, 6807, 21, 11, 12); 10 runs (24, 8985, 21, 17, 10); 4 pools (9, 2900, 17, 6, 8); 1 glide (1, 1095, 12, 2, 1). Within habitat type, we noted the generality of invertebrate group plasticity for microhabitat combination types both within and between stream reaches. Also, certain invertebrate groups did show relatively large numbers of individuals in particular microhabitat combination types despite relatively low statistical contributions to associations.

PP127 - A Comparison of the Effect of Historic Land Use and Present Day Land Cover on Fish Populations and Diversity in Anderson County, South Carolina

Emma Clayton, Dennis Haney

Furman University, Greenville, SC

The effects of historic land use and present day land cover are often so ubiquitous that they go unnoticed. However, the impact of legacy land use can be seen in both terrestrial and aquatic habitats. Some historic land use practices date back decades, or even centuries. Through correlation analyses of present and historic land use with current biotic data, water chemistry, and geomorphology data, we assessed the impact of both present-day and historic land use on fish populations and diversity. Focusing on streams in Anderson County, SC, evaluated these variables though a joint lens of biology and history. Using Spearman's correlations, we found species richness had a significant negative correlation with percent impervious surface cover ($\rho = -0.58$) and percent urban cover ($\rho = -0.53$). Historic acres of cotton had a significant positive correlation with entrenchment ($\rho = 0.48$), but was negatively correlated with Simpson's diversity ($\rho = -0.55$). Historic total acres of crops had a significant positive correlation with entrenchment ($\rho = 0.48$). Given both present and historic land cover data were significantly correlated with alterations in stream habitat and fish populations, the most successful restoration efforts should take into account the alleviation of factors from historic and present-day land use practices.

PP128 - Microbial Assemblages in Relation to Host and Environmental Surroundings

John Hoverson, Mark Fischer, Gabriel Hooper, Nathan Edmondson, Kyle J. Harris, Matthew Becker

Liberty University, Lynchburg, VA

Communities of bacteria inhabit almost every habitat on the planet, from human digestive systems to freshwater bodies. In addition, there is an ever-expanding realization of the importance of microbiomes to the health of associated organisms. Microbes play a fundamental role within freshwater ecosystems as they influence stream health and interspecies relationships, providing support for an organism and environment's health. As a host to various epibionts in freshwater streams, crayfish have been shown to provide a unique habitat for bacterial and annelid ectosymbionts (branchiobdellidan worms). This project will focus on the microbial assemblages in the environment (water and substrate) along with two microsites (ventral abdomen and gill chamber) on *Cambarus spp.*of crayfish where branchiobdellidan worms (BWs) are commonly found.

Recent findings in this lab have revealed a significant difference in the microbial community assembly (MCA) of varying sample types (water, substrate, and crayfish), but this experiment will also compare microsites on the crayfish (ventral abdomen and gill chamber) with the environment (water and substrate). The MCA will be assessed with DNA fingerprinting of the 16S gene and next generation sequencing followed by QIIME2 bioinformatics analysis. We expect to find that the a-diversity of the crayfish MCA in relation to the surrounding environment (water and substrate) to be significantly different (corresponding to previous experimental findings). We also expect that the MCA a-diversity of the crayfish microhabitats (ventral abdomen and gill chamber) to be significantly different from one another with the ventral abdomen being more closely associated with the substrate and the gill chamber MCA being more closely associated with the water. The purpose of this project is to enhance the broader understanding of freshwater ecosystems due to the interactions among BWs and the MCA on crayfish and the MCA associated with the environment.

PP129 - Profiling Bat Species Activity at Different Artificial Light Intensities

Taylor Bryan, Thomas McElroy

Kennesaw State University, Kennesaw, GA

Human intervention in most ecosystems across the globe is causing unprecedented change with urbanization having major impacts on bat activity and species disbursement within a community. The nocturnal nature of bats suggests that the increase in light pollution over the past years likely affects bat activity leading to the question of how bats respond to artificial lighting. Some studies have examined what effects artificial light intensities have on bats through species activity and insect availability. Documenting bat species presence and activity at different artificial light intensities may reveal bat species that benefit from artificial light and if some bat species are negatively affected. The three study sites were located in a highly urbanized area within a one-mile radius of each other. The Publix shopping center parking lot represents high artificial light intensity (48-72 lux); the apartment complex parking lot represents low artificial light intensity (5-12 lux); the KSU Field Station represents no artificial light presence (0-1 lux).

We found significant differences in bat activity levels among the sampled areas. There were also significant differences among species percent presence among areas overall. This was a preliminary data analysis with a relatively small sample size. The data indicated differences among the sampled locations. The differences in species presence and activities may be related to light levels at the different sites; however, light level may not be the only factor driving the detected differences between the sites. Future work should include multivariate analysis of other data variables, such as weather conditions, seasonality, canopy density measurements, roost availability, access to water, and more comprehensive prey abundance counts for the sampled sites. Further manual confirmation of bat species auto-identification labels provided by Wildlife Acoustics® Kaleidoscope Pro 4.0.0 will be continued and may change species presence as well as bat pass data.

PP130 - Species Inventory and Monitoring of Pollinators Along the Blue Ridge Parkway

Breana Cook, Drew Milavec, Sierra Harwood, Jennifer Geib

Appalachian State University, Boone, NC

Pollinators are needed to sustain ecosystems and are significant environmental servicers. Recent studies provide evidence of declines and range contractions among some species sparking the need to inventory native species for future conservation work. The Blue Ridge Parkway Pollinator Project aims to inventory native pollinators, particularly bee species, along the roadway throughout North Carolina and Virginia. Sixty inventory sites along 469 miles of roadway were managed by teams comprised of Appalachian State students (15 sites) or Citizen Scientists (45 sites). Specimens at each site were collected every other week from April through mid-October 2019,using passive glycol traps and optional netting surveys. This inventory is the most extensive of its kind in Southern Appalachians. Preliminary processing of specimens indicates a diverse array of native species; non-native *Apis mellifera* are also abundant in most areas. We expect to see location-specific species as well as generalists who can be found throughout the parkway. Data from the project will allow mapping of species distributions and abundances, population genetic studies, identification of species of interest and/or concern for conservation targets, and educational outreach.

PP131 - Temporal population genetics of invasive Asian Swamp Eels (Monopterus albus) in Georgia

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There are currently five known populations of Asian Swamp Eels (*Monopterus albus*) in the United States. Three populations are located in Florida, one population in Hawaii, and one population in Georgia. The introduction of the eels is likely due to the large market for Asian Swamp Eels as a food fish or as part of an aquarium release. The swamp eels occupy a similar trophic position as *Gambusia* sp., an insectivorous fish, impacting the food web and creating competition for resources for native insectivorous fishes in the Chattahoochee River. The first continental U.S. population was documented in 1994 within several ponds at the Chattahoochee Nature Center, a private nature preserve in Roswell, Georgia. Because the swamp eels are obligate air breathers and are able to burrow into the muddy substrates, research activity on this population has been limited. In order to obtain samples from the current population, we used backpack electrofishing and leaf litter traps. Using samples from previous research projects and the current samples, we are using molecular tools to compare the Chattahoochee Nature Center population from 1998, 2017, and 2019/2020 to assess changes in the population genetics of the population over time. Using 8-10 microsatellite markers, we plan to assess changes in heterozygosity and allelic richness and look for unique alleles in the recent samples that may suggest additional introduction events after the initial founding of the population. Alternatively, isolation of the population may have led to a decline of genetic diversity.

PP132 - Seed Bank Densities and Composition of Forest Edge and Understory Sites

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Soil seed banks from a forest understory and a forest edge at the Wingate University Campus Lake at Wingate University in Wingate, North Carolina, were investigated to compare species composition and seed density. This came about due to earlier observations which showed that no herbaceous plants were found in the forest understory whereas several herbaceous plants were present along the forest edge. Soils were randomly collected in November 2019 after seed rain had occurred along a forest edge and corresponding understory in the same tree stand. Five 0.5 m^2 plots were randomly selected along the forest edge as well as in the forest understory. Five soil cores (28.3 cm^2 each) were collected from each plot to a depth of 5 cm, one taken at each corner of the plot and one taken from the center. Soils were stored in polyethylene containers with lids at 5°C in a Percival incubator and were exposed to 24-hour dark. Soils were sieved to determine seed presence using five mesh sizes. Soil in each sieve was reviewed using a dissecting scope at 7.5x magnification to aid in identification. The average seed density of the forest edge was determined to be 18,115 seeds/m^2. The average seed density of the forest understory was determined to be 6,408 seeds/m^2. A single species comprised 81.8% of the forest edge seed density and 77.9% of the forest understory seed density and was the only species found in every soil core from both the edge and understory core samples. Twenty-three species were found in the edge and thirteen species were found in the understory with ten species overlapping. These data suggest that absence of plants in the understory may be due to a smaller seed bank and lower species diversity when compared to the forest edge.

PP133 - Bacterial Flora and Insects Detected in Guano from Several Local Species of Bats

Shannon Whitney, Thomas McElroy

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Bat diversity in northwest Georgia consists of 16 insectivore species. These bat species consume similar food resources, so ecologists wonder how these bats deal with interspecies competition. A known way of reducing interspecies competition is by partitioning the resource available, however this implies that bats are actively selecting certain prey instead of feeding on whatever is available. Collecting data to support or reject this hypothesis is difficult to obtain. Bat feces was collected from 105 individuals (6 different species) from the area around Rome, GA. With the use of NextGen Sequencing (NGS) we are able to collect DNA from fecal material and determine what each bat is consuming. This method serves as a noninvasive measure to profile a bat's diet and even to identify what species the sample came from. The data collected indicates differences in diet among bat species and seasonal shifts.

Future work will require multifactorial approaches to establish a relationship between diet shifts and spatial/ temporal feeding behaviors, or to discriminate between optimal foraging models vs. marginal value theorem predictions. This study also looked at bacteria present in the guano samples as an initial report on the bacterial diversity in guano from local bat species. Difference in bacterial diversity among species and temporal samples may be related to differences of host species, diet and other physiologic or morphologic characteristics of the bat species. To the best of our knowledge, this first report on bacterial communities in bat guano collected in Northwest Georgia, USA. This stirs scientific interest for possibilities of isolating and characterizing novel bacteria with multiple functions for production of antibiotics or other purposes.

PP134 - Reproductive Effort and Output Within and Between Two Species of Pitcher Plant (*Sarracenia*)

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Sarracenia jonesii (Jones' pitcher plant), a federally threatened species, is sometimes outplanted into sites where its congener *Sarracenia purpurea* var. *montana* (mountain purple pitcher plant), a federal species of concern, grows. However, anecdotal evidence, and grey literature from breeders, suggests that species distinctions within this genus are maintained primarily through allopatry, and that plants in sympatry hybridize readily. Observations of phenotypic hybrids at sites where these species co-occur, and genetic confirmation of hybrid parentage, led us to ask about the potential for, and realization of, interspecific breeding. In summer 2019, we monitored *S. jonesii* and

S. purpurea var. *montana* at two sympatric western North Carolina field sites. Parental species and their phenotypic hybrids were visited weekly during the flowering season to assess plant phenological stages and to collect anthers for pollen viability analysis; ovaries were collected after floral senescence to analyze seed production, seed viability, and seed germinability. Results revealed significant overlap in flower production and receptivity, and showed that pollen from both species maintained high viability even after anthers were shed. Parental species and their hybrids all produced large numbers of seeds; viability of these seeds is being assessed. These data demonstrate the potential for hybridization between two species of conservation concern under field conditions, and suggest that interventions such as floral bagging should be undertaken to restrict gene flow across these permeable species boundaries. Future investigations will compare parental species' seed production in sympatry vs. allopatry, and will discern parental versus hybrid status of the seed generation.

PP135 - Factors Contributing to Reproductive Success and Failure in Virginia Spiraea (*Spiraea virginiana*), a Federally Threatened Shrub

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Virginia spiraea (*Spiraea virginiana*) is a perennial shrub with both sexual and asexual modes of reproduction, found in riparian habitats throughout the Appalachian Mountains. The species was listed as federally threatened in 1990 due to hydrologic disturbance, and populations might suffer from inbreeding depression. In this series of experiments, we examined factors that could challenge the species' survival. We compared reproductive effort and output among populations, manipulated breeding systems to see their effects on seed production, identified insect visitors to ascertain potential pollinators, used physiological measurements in experimental gardens to determine whether the species is shade-tolerant, and tested the potential for hybridization with Japanese spiraea (*Spiraea japonica*), an invasive congener. Results showed variation in reproductive effort and seed production among genetic individuals and populations, and analyses of breeding systems are ongoing. Guilds of insect visitors varied widely in their potential pollination roles; because Virginia spiraea pollen loads were negligible in ants and flies, it is likely that other groups (beetles, bees, wasps) are the plant's major pollinators. Virginia spiraea's photosynthetic rate did not saturate until full light, and unshaded plants produced more corymbs, suggesting that removal of woody species could increase the species' performance under field conditions. Finally, although reproductive effort was high in Japanese spiraea, cross-pollinations between native and invasive spiraea produced no seeds. Results will inform efforts to restore and augment populations of Virginia spiraea throughout its range, and will ensure the continued persistence of existing clones.

PP136 - Assessing the Health of Gray's Lily (*Lilium grayi*) Populations with Demographic Monitoring

Ben Brewer, Matt C. Estep

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Lilium grayi S. Watson, Gray's Lily, is a threatened perennial herb endemic to high elevations in the Southern Appalachians of Virginia, North Carolina, and Tennessee. *L. grayi* is an iconic species in the grassy bald plant community, and also grows in mesic forests and meadows. L. *grayi* faces multiple challenges, including disease caused by a fungal phytopathogen and loss of genetic diversity due to potential hybridization with sister species *L. canadense*. Lily Leaf Spot (LLS) disease results in early senescence of aboveground tissues, and often prevents individuals from reproducing successfully. Early season collapse resulting from LLS is evident at a large scale in the remaining populations of *L. grayi*, with differing severity in different environments. Demographic monitoring of *L. grayi* is necessary to fully understand how the disease is affecting populations. During the summer of 2019, nine 25m^2 plots were established in different plant communities at the Tater Hill Plant Preserve, Watauga County, North Carolina, to monitor flowering *L. grayi* individuals for reproductive success. Data was collected on plant size, severity of disease infection, shading strata, and reproductive output. The Tater Hill data was analyzed in concert with similar data collected from individuals at Grandfather Mountain, North Carolina. For all individuals, an average of 27% of flowers successfully produced fruit, compared to 33% at Tater Hill and 8% at Grandfather Mountain. When considering plant community, 63% of flowers in the grassy bald community produced fruit compared to 9% of flowers in forest communities. These results suggest that reproductive output is low for all members of the species, especially for individuals in communities with a closed canopy cover. Demographic monitoring will continue during the summers of 2020 and 2021 to collect additional data, in addition to sampling individuals to perform a survey of genetic diversity.

PP137 - A study of the biodiversity of small mammal populations in the Orders of Rodentia and Chiroptera across various habitats and seasons.

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A mammal survey was conducted in two locations in Panama (a cloud forest in central west Panama and an island off the SW Pacific Ocean coast of Panama) in order to examine biodiversity. Both locations have had sparse research conducted and little documented fauna. Specimens were observed and/or trapped using Tomahawk traps, standard Sherman live traps, mist nets, and camera traps. A total of 107 specimens representing 14 species were collected from the survey area. The species collected included *Handleyomys alfaroi, Zygodontomys brevicauda, Nyctomys sumichrasti, Tylomys watsoni, Peromyscus nudipes, Heteromys desmarestianus, Orthogeomys cavator, Reithrodontomys sp., Artibeus toltecus, Dermanura incomitata, Artibeus lituratus, Carollia sowelli, Carollia castanea, Sturnira luisi, and Sturnira hondourensis.* A comparison of ecological samples showed the effects of seasons on small mammalian diversity in highlands. Interestingly, surveyed individuals of Rodentia increased in species diversity during the wet season, whereas Chiroptera increased in species diversity during the dry season. Five specimens with unmatched DNA sequences indicate identification of two new species: *Nyctomys sp.* and *Reithrodontomys sp*.

PP138 - Predictive niche modeling for the identification of cotton, corn, and grape pathogens of greatest concern in Texas

Christopher Randle, Nicholas Reger, Jiajun Hoo, Laura Bianchi, Justin Williams

Sam Houston State University, Huntsville, TX

As a border state experiencing both heavy traffic in foreign imports and serving as the nation's second-leading agricultural producer, Texas is particularly vulnerable to invasive crop pests and pathogens. Further, as a large state experiencing north-to-south and east-to-west variation in climate, soils, and vegetative cover, Texas potentially provides a wide range of suitable habitat in which crop pathogens and pests could persist, and from which they could be transported to the croplands of neighboring states. Corn, cotton, and emergent viniculture are identified as leading areas of agricultural concern in the state of Texas. Ecological niche models allow prediction of habitats suitable for pest and pathogen persistence in Texas given occurrence and bioclimatic data from their native range. In this study, ecological niche are used to project areas of Texas in which habitats are suitable for colonization by non-native pests and pathogens of corn, cotton, and grapes for the purpose of 1) identifying global hotspots from which pests and pathogens are most likely to be transported to Texas, 2) ranking pests and pathogens from greatest to least concern for persistence in Texas croplands and natural habitats, and 3) identifying areas of Texas most likely to serve as suitable habitat to dangerous pests and pathogens.

PP139 - Defining the Freshwater Sponge Diversity in Louisiana: Wallace Lake Provides an Ecological Niche for Defined Species

Charmaine Smith, Quinton Moore, Mary Miller

Baton Rouge Community College, Baton Rouge, LA

The diversity of freshwater sponges in Louisiana was last defined in 1968, as part of a dissertation study by Michael Poirrier. Knowing the importance of freshwater sponges as an environmental health indicator, it was important to conduct an extensive survey and provide locations that were evident in species richness and abundance. Since June 2019, 147 freshwater sponge samples were collected from 60 sites, across 36 parishes. The sponges were described based on their spicule and gemmule morphology using standard light microscopy and SEM, along with DNA barcoding. Water samples from each site were analyzed for turbidity, dissolved oxygen, pH, conductivity, and 14 water quality indicators. From this study, an average of five sponge samples was collected from each site with the diversity consisting of one or two species. Wallace Lake Dam, in Caddo Parish, was recognized as the most diverse site with 15 samples collected, and 4 species identified. The growth substrate availability and water parameters measured, provide an indication of optimum ecological requirements for freshwater sponges in Louisiana.

PP140 - Analysis of eDNA from aquatic environments to detect the walking catfish (***Clarias batrachus)***

Using environmental DNA to detect the walking catfish (Clarias batrachus) in South Florida Waterways
Robert C. Gutierrez, Karen Morejon, Samantha Sierra, Dr. Meade, and , Dr. Laberge

Abstract

Invasive species are pervasive in the Florida ecosystem and currently there is an increased number of displaced native species. The walking catfish (Clarias batrachus) is an invasive species that has been found in South Florida. Due to it's ability to move from one pond to another, it has spread throughout the freshwater system in South Florida. The voracious nature of the walking catfish has allowed it to outcompete the local Florida fish fauna. Using the ANDe Smith-Root eDNA sampling backpack we filtered water from our local waterways extracted eDNA (environmental DNA) in order to identify types of species present at the sampling site. Our focus is to locate the bodies of water where the invasive walking catfish have spread in order to monitor and control their spread within the Florida ecosystem. We can confirm the presence of species identified by eDNA by electro fishing with the APEX Smith-Root backpack. For comparison, we have extracted the DNA of a walking catfish that we captured and compared it with the eDNA that was filtered out of the water. We used PCR to amplify the mitochondrial gene Cytochrome Oxidase I that is normally used in DNA barcoding. Currently we have only located one live walking catfish in Amelia Earhart Park, but we are continuing to sample local waterways like Snake Creek Park and Miami Lakes and sampling eDNA from filtered water at these sites. In the future we hope to not only use these techniques to find invasive species but to also locate endangered species or to just catalog fish in a certain body of water much more efficiently.

PP141 - Modeling Population Dynamics and Management of an Invasive Japanese Barberry Population in the Southern Appalachian Mountains

Christian Brown, Jennifer Geib

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Through transportation by humans, plant species are able to travel once impossibly far distances in a short period of time. These species can establish themselves in foreign environments and may become detrimental to the native species or to crops cultivated by humans. *Berberis thunbergii*, Japanese barberry, is one such plant which disrupts the ecology of native ecosystems in the United States. The aim of this project was to create an ecological stage-based model which can aid in elucidating the ideal method of elimination for an invasive population of Japanese barberry. Using data found in the literature, I created a Lefkovitch matrix model in order to predict the growth rate of a Japanese barberry population located in Appalachian State University's nature preserve. I also performed an elasticity analysis on this model which yielded the proportional contribution of each life stage to the growth of the population. I found that 3 stages, seeds, seedlings, and plants with 1-3 stems had the greatest influence on the growth of the population. I simulated four management methods by altering values in the original stage-based matrix model. The first three simulations targeted each of the three influential stages individually and the fourth combined all three of the alterations made in the previous simulations. Only the simulation which targeted all three influential life-stages of the Japanese barberry population produced a negative growth rate for the population, while the other three

simulations yielded positive population growth rates, albeit the values were reduced when compared to the original matrix model. These results can be used to inform management strategies aimed at eliminating the invasive Japanese barberry population in an efficient way.

PP142 - Diverse leaf color phenotypes of cranefly orchid, *Tipularia discolor*

Emily Gonzalez, Nicole Hughes

High Point University, High Point, NC

Leaves of the terrestrial, wintergreen orchid *Tipularia discolor* exhibit a striking range of leaf color and texture phenotypes, which are thought aid in herbivory deterrence of camouflage. The purpose of this study was to document the breadth of diversity found in natural populations of cranefly orchid growing in the piedmont of North Carolina, as a preliminary step towards determining their patterns of inheritance via traditional crosses. Distinct leaf color patterns observed on adaxial (upper) surfaces included: solid green epidermis, solid purple epidermis, silver/grey flecks beneath the upper epidermis, purple epidermal spots of various sizes, yellow streaks, and textural "warts" of various sizes; more often than not, leaves expressed combinations of two or more of these features simultaneously. Abaxial surfaces also differed between individuals, either appearing solid purple, solid green (absence of purple), or an intermediate hue. We have observed almost all of these phenotypes return on the same plant year after year, even when light, fertilizer, and water are controlled for in a greenhouse setting. However, this has yet to be verified for a few of the more newly-identified phenotypes, including yellow streaks and white spots. Next steps will be to conduct crosses between individuals to look for patterns consistent with Mendelian inheritance.

PP143 - Seed viability and germination success of *Spartina alterniflora* in Georgia salt marshes

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Georgia Southern University, Savannah, GA

Spartina alterniflora is the dominant coastal salt marsh plant species along the East Coast of the United States and plays a critical role in marsh growth and maintenance. Information on *S. alterniflora* phenology and fecundity for an area is vital in coastal salt marsh management strategies, but there is little data on seed viability and germination success for *S. alterniflora* within Georgia salt marshes. The aim of this study was to assess seed set, seed viability, and germination success for *S. alterniflora* collected from three salt marshes in Chatham County, Georgia. Specifically, phenological status (i.e., flowering and fruit status) was monitored for randomly selected individuals within each marsh bimonthly in September and October 2019, and mature spikelets, when present, were collected. Spikelets were processed shortly after collection, number of seeds/spikelet was counted, and seeds were placed in cold wet conditions for 2-3 months to break dormancy. Beginning in January 2020, seed viability will be tested for each collected spikelet using the tetrazolium red (TZ) dye test, and germination will be monitored for seeds maintained in glass culture dishes. Results from this study will provide critical information to coastal managers on the current status of populations of *S. alterniflora* in Georgia salt marshes.

PP144 - Genetic Diversity and Population Structure in Porter's Sunflower (*Helianthus porteri*): Granite and Sandstone Outcrop Populations

Amber Rittgers, Christian Hull

University of North Georgia, Oakwood, GA

Helianthus porteri (Porter's sunflower) is an annual forb near-endemic to granite outcrops in the Southeastern Piedmont. Within the last 30 years *H. porteri* has also been observed naturally occurring within Alabama's Valley and Ridge province, growing on sandstone outcrops. Distributed among disjunct and edaphically controlled habitats with the Talladega Mountains as a geographic barrier between the Piedmont and the Valley and Ridge provinces, we expect to find a high genetic variation between the granite and sandstone populations. We have isolated total genomic DNA of *H. porteri* from seven sandstone populations and six granite populations (n = 255) located in eastern Alabama. Using 18 simple sequence repeat (SSR) markers, we aim to compare the genetic variation and population structure among these 13 populations. Previous research has shown the granite outcrop populations of *H. porteri* in three other southeastern states to have a high genetic diversity and low population structure. Future analysis will look at the genetic diversity of *H. porteri* between regional populations, as well as possible substrate effects.

PP145 - Assessment of the Resiliency and Status of Endangered Apalachicola Rosemary, *Conradina glabra* Shinners (Lamiacae)

Amber Rittgers

Atlanta Botanical Garden, Atlanta, GA

Apalachicola rosemary (*Conradina glabra* Shinners) is a rare perennial shrub endemic to the xeric sandhills east of the Apalachicola River in Liberty County, Florida. *Conradina glabra* is federally endangered due to habitat destruction and modification resulting from incompatible forest management practices that further impact this species' narrow distribution. Currently, there is only one known 1,000 ha area population recorded. To assist species recovery, the U.S. Fish and Wildlife Service and the Atlanta Botanical Garden aim to maintain a reproductive and genetically diverse population. One outstanding question is whether *C. glabra* is primarily clonal or is reproducing sexually *in situ*. Using population genetic analysis, we are testing for clonality and the extent and structure of genetic diversity in *C. glabra* so that targeted conservation efforts may be applied. Individual plant samples (n=745) were collected from 15 restoration zones in Torreya State Park utilizing two sampling schemes in March of 2019. We isolated genetic material from each sample for genotyping by RADSeq technique. Future analysis of single nucleotide polymorphisms (SNP) may provide insight on *C. glabra's* genetic diversity and species resiliency by characterizing variation and clonality.

PP146 - Phenotypic plasticity of *Hydrocotyle bonariensis* across environmental gradients on two southeastern (USA) barrier islands

Micah Burks, Joseph Watson, Thomas Hancock

Middle Georgia State University, Macon, GA

Hydrocotyle bonariensis Lamarck is a C_3 perennial rhizomatous species that grows from Virginia (USA) to Chile and is commonly found on barrier islands of the southeastern United States. *Hydrocotyle bonariensis* has the unique ability to grow across a range of barrier island habitats. These habitats represent a gradient of environmental stresses that the plant must endure. The purpose of this study was to investigate the morphological and anatomical response of *Hydrocotyle bonariensis* to the unique microenvironments present in barrier island systems. Two field sites were selected for study, Fort Fisher, NC and Sapelo Island, GA. At both sites, subsurface sand temperatures, photosynthetically active radiation (PAR) and rain measurements were taken using data loggers. Above ground structures of *H. bonariensis* plants were collected from specific habitats at both study sites. These samples were returned to the laboratory for analysis. Analysis included measurements of petiole length, leaf area, stomatal frequency and leaf tissue layer thickness. Although as a whole both Sapelo and Fort Fisher experienced similar temperatures, sunlight and rainfall, there were large differences in subsurface sand temperature and PAR measurements across habitats within each site (microsite differences). Between site differences in plant characters were small, however within site differences were appreciable. Leaves of plants growing on the frontal dunes were smaller, thicker and had more stomata/mm^2 than leaves growing in the shrub zone. Leaves of plants growing in the habitats between the frontal dunes and shrub zone demonstrated intermediate leaf characters. *Hydrocotyle bonariensis* is one of the few plants that grows across the entire range of barrier island habitats. The ability to survive in a variety of microsites is due in part to the morphological and anatomical phenotypic plasticity of *H. bonariensis*.

PP147 - The cutaneous microbiomes of Appalachian salamanders and their r ole as an innate defense against the pathogen *Batrachochytrium dendrobatidis*

Magdalene Lederer, Miranda Sheridan, Matthew Becker

Liberty University, Lynchburg, VA

In recent years, amphibian populations worldwide have seen unprecedented declines, which have been associated with a dramatic increase of chytridiomycosis. *Batrachochytrium dendrobatidis* (*Bd*) and *B. salamandrivorans* (*Bsal*) are two fungal pathogens that infect the skin of amphibians, leading to chytridiomycosis. Previous research suggests that the symbiotic microbial skin community of some amphibians protects them from *Bd* and *Bsal*. Considering these results, we characterized the microbial communities of two stream salamanders, *Desmognathus fuscus* and *D. monticola,* and examined interactions between the isolated microbes and the pathogen *Bd*. We captured *D. fuscus* (n=18) and *D. monticola* (n=11) individuals from a stream in Bedford County, VA. We rinsed all salamanders to remove transient microbes before swabbing them to collect microbial cells. These were transferred to R2A agar and incubated at room temperature. We identified unique morphotypes by extracting, amplifying, and sequencing the 16S rRNA gene. We co-cultured each isolate with *Bd* to determine if they promote inhibition or growth of *Bd in vitro*.

We found that *D. fuscus* and *D. monticola* had similar microbial community compositions, primarily dominated by the phyla Proteobacteria (61% of isolates), Actinobacteria (18%), Firmicutes (18%), and Bacteroides (3%). These communities were phylogenetically diverse, containing 34 genera of bacteria. The dominant genus was *Pseudomonas*. We cultured an average of 16 and 15 isolates per *D. fuscus* and *D. monticola*, respectively. Few isolates (2.5%) inhibited *Bd* in an *in vitro* challenge assay. This percentage is lower than reported in previous studies, suggesting that these species may have other defenses against *Bd.* It is unclear how *Bd* affects *D. fuscus* and *D.* monticola at the individual and population levels, but there are no reports of drastic die-offs, as have been seen in affected species. Antifungal cultures isolated from this study could be used potentially as probiotics to mitigate chytridiomycosis in susceptible species.

PP148 - The characterization of the microbiome for the Northern two-lined salamander (*Eurycea bislineata*) and its ecological interactions with the pathogen *Batrachochytrium dendrobatidis*

Kristen Enns, Olivia Beiler, Nicholas Minner, Matthew Becker

Liberty University, Lynchburg, VA

Fungal pathogens are a major threat to amphibians worldwide, but the most prevalent fungal pathogen is *Batrachochytrium dendrobatidis* (Bd). Bd is a chytrid fungus that is highly virulent and has been linked to population decline in numerous amphibian populations across the world due to the development of chytridiomycosis. Bd infects the amphibian's skin by rooting their spherical thalli into the amphibian's keratinized epidermal layer of their skin, disrupting the exchange of many vital molecules such as oxygen, carbon dioxide, and ions. The focus of this project was to characterize the skin microbiome of the Northern two-lined salamander. The resident microbiome of an individual is intricately linked to its survival and overall health due to its role in metabolism, the immune system, and in defense. It has been demonstrated that the microbiome plays a vital role in pathogen-host interactions, so it is vital to better understand the role that the microbiome plays when it comes to preventing pathogens, such as Bd. This project focused on describing the microbiome of the Northern two-lined salamander by collecting swabs from individuals caught along the Blue Ridge Parkway. All bacterial samples were isolated on R2A media and the 16S rRNA gene was extracted using a freeze-thaw technique. Once the DNA was extracted, a PCR was run, and samples were sent off for sequencing. We are currently, using sequences to identify each unique morphotype that was cultured on R2A. The hope is that this project is to act as springboard for future work when bacterial isolates can be used in a challenge assay against Bd in hopes of finding bacterial strains that inhibit the fungal pathogen.

PP149 - Comparative Analysis of the Cutaneous Microbiome of Two Sympatric Cryptic Salamander Species

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The microbiome of amphibian skin has received considerable research attention over the previous two decades. Our understanding of the influence microbial communities has on host life history, ecology, and evolution has led to the understanding that organisms and their microbial communities should be considered as composite units of evolution. Previous research has indicated the existence of differences in cryptic, sister-species in the frequency of occurrence of cutaneous parasites despite extreme similarity in habitat and behavior. These differences may indicate the existence of biochemical differences between the two species. Such differences would necessarily impact the cutaneous microbiome. We sampled and assessed the cutaneous microbial flora of two sympatric, cryptic, sister-species, *Desmognathus quadramaculatus* (Black-bellied Salamander) and *D. folkertsi* (Dwarf Black-bellied Salamander). Whole genomic DNA was isolated using Qiagen PowerSoil Pro Kit with a modified protocol. We amplified the V4 region of the 16S rDNA gene using the 515F/1806R primers with 2X250 paired-end sequencing. Additionally, DNA samples were taken from soil, water, and air for comparative purposes. A total of 28 million 16S rDNA sequences were generated using an Illumina sequencer with NextGen techniques. Analysis of cutaneous microbiome assemblages are discussed.

PP150 - Database Analysis of Novel, Lead Compounds that Inhibit Biofilm Production in *Bacillus subtilis, Escherichia coli, Pseudomonas aeruginosa, Staphylococcus aureus,* and *Streptococcus mutans.*

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Bacterial resistance to antibiotics has become a serious threat to modern medicine. Traditional antimicrobials work by killing bacteria or inhibiting bacterial growth, and due to bacterial rapid reproductive rates and overuse of traditional antibiotics, resistant bacteria are quickly selected. Therefore, alternative treatments must be explored. A potential target is bacterial communication pathways that lead to biofilm formation. Biofilms are extracellular matrices that provide a protective environment for the bacteria, including avoidance of the host immune system. Gene expression for biofilm formation is controlled by a communication system that utilizes quorum sensing: bacteria recognize a threshold level of signaling molecules called autoinducers and then a response ensues. By synthesizing small compounds which resemble autoinducers, we hope to competitively inhibit the pathways responsible for the formation of biofilm in order to decrease the selection of antibiotic-resistant bacterial strains.

Carboxylic acid derivatives were coupled to amino acids through a dehydration synthesis to produce families of novel lead compounds. Biofilm inhibition was measured via a traditional crystal violet assay. The results collected were compiled into a comprehensive database organized by species and compound families. To date, over 300 compounds have been tested for biofilm inhibiting capability. Of those 300 compounds, 28 have been confirmed to inhibit biofilm formation without utilizing bactericidal or bacteriostatic properties. Compounds containing variations of halogenated functionality centered around aromatic rings, in addition to trans-cinnamic acid derivatives, have been found to possess anti-biofilm properties in *Bacillus subtilis*, *Staphylococcus aureus* and *Streptococcus mutans*. Over 100 additional compounds will be analyzed and added to the database to confirm the trends. In addition to being useful for designing new novel lead compounds, the database in combination with genetic analyses may allow the connection of compound structures to a specific pathway in biofilm formation: the signal transduction cascade or the construction of biofilm.

PP151 - The Importance of Compliant Contact Lens Care

Todd Wood, Tyler Collins, Sonya Anderson, Charles Asouzu, Brittany Burhenn, Preston Harris, Allison Hay, Jim Lewis, Kierra Mercer, Duaa Mohamed, Abby Grace Moore, Abbie Otto, Shivani Patel, Aaliyah Robinson, John Rodriguez, Tyler Tolbert, Charlene Ubah, Alexandrea Whitmore, Lauren King

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Silicone hydrogel contact lenses are the leading type of contact lens on the market today, but there are significant problems associated with their use in the form of bacterial keratitis. It is common for contact lens care to include antimicrobial solutions, but ocular pathogens' ability to produce biofilm may inhibit antimicrobial function. In this study, we examined how treating silicone hydrogel contact lenses with lens care solutions before exposure to bacteria, after exposure to bacteria, and with a regimen that is fully compliant with manufacturer standards of contact lens care affects the ability of *Staphylococcus aureus* to adhere and grow on contact lenses. Treatments included Biotrue, Opti-Free Puremoist, and Equate contact lens solutions, as well as lysozyme, an antimicrobial enzyme produced by the innate immune system in the eye. Bacteria adhered to the contact lens after treatment and washing were quantified via dilution and plate count. Pre-treatment with contact lens solutions did not affect the ability *of S. aureus* to adhere or grow on the contact lenses, resulting in no statistical difference from an untreated control. Post-treatment also displayed no significant difference between treatments and control. Upon addition of a fully compliant contact lens care regimen to the post-treatment group, which included all three steps explicitly listed by the manufacturer's protocol, a statistically significant decrease in viable bacterial counts from control was observed. In conclusion, *S. aureus* demonstrated robust growth on the silicone hydrogel contact lenses, and treatment with contact lens solutions was unable to prevent bacterial adherence or growth on the lens. These results demonstrate the importance of strict compliance to the manufacturer protocol in contact lens care.

PP152 - Investigation of unknown microbes discovered in nicotine-treated water housing experimental zebrafish

Amanda Harless, Sharon Keller, Wendy Dustman, Lee Kurtz, Gabriella Tyler, Rebekah Ward, Cindy Achat-Mendes, Robert Haining

Georgia Gwinnett College, Lawrenceville, GA

In a zebrafish model test environment, in which the potential neuroprotective effects of nicotine were being investigated, an unexpected blue coloration was observed in the water. This product turned the water from a normal clear color to a striking blue within 24 hours. Behavioral observations indicated no untoward effects of water coloration on zebrafish. Samples were taken from the water and placed on agar plates in anaerobic environments using spread plate techniques. Two pure isolated colonies were found from the samples and defined as two different microbes based on morphology and smell. Based on literature research, it is hypothesized that these organisms are related to *Paeanarthrobacter nicotinovorus,* which are nicotine-degrading microorganisms. DNA was extracted and PCR was performed on the two isolates. The PCR products were then sequenced to determine if these organisms have any relations to *Paeanarthrobacter nicotinovorus*. Identification of *Paeanarthrobacter nicotinovorus* that can thrive amongst a robust zebrafish population has implications for its utility in studying the metabolic pathway of nicotine metabolism and its potential environmental impact in nearby lakes and streams.

PP153 - Bacteriophage Research: Phage Hunting and Genome Annotation

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The SEA-PHAGES (Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science) research program is an international project hosted by the Howard Hughes Medical Institute in collaboration with HHMI Professor Graham Hatfull at the University of Pittsburgh. One aim of the program is to increase undergraduate interest and retention in the biological sciences through immersion in authentic research. Bacteriophages ("phage") are viruses that infect and replicate inside bacteria and are the most abundant biological entities on the planet. Phage have captured the interest of scientists because of their potential - from gene therapy to the treatment of bacterial infections. The first of the two SEA-PHAGES courses focused on the isolation, purification, and amplification of bacteriophage collected from soil using the bacterial host *Arthrobacter globiformis*. It is highly likely that any soil sample containing bacteria will also have phage, although much less likely to have phage that can infect any given species of bacteria. I successfully isolated a bacteriophage, Persistence, that infects *A. globiformis*. Following isolation, Persistence, was purified and amplified to create a homozygous population of high-titer phage. A sample of Persistence was submitted to the Augusta University Electron Microscopy Core Laboratory for transmission electron microscopy (TEM) and to the University of Pittsburgh for archiving. DNA was extracted and submitted to the Pittsburg Bacteriophage Institute for sequencing. The Persistence genome will be annotated in the second SEA-PHAGES course, taking place this semester.

PP154 - Antibiotic Production and Identification of Bacteria Isolated from Soil and Peat Samples

Tyler Pikes, Randall Harris

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Antibiotics have revolutionized medicine and saved millions of lives. They are a form of medicine that inhibits the growth of or kill bacteria, but the fast emergence of antibiotic resistant bacteria happening worldwide is affecting the efficacy of these drugs. Because about 75% of antibiotics in clinical use are derived from soil bacteria, the objective of this study was to examine environmental bacterial isolates for antibiotic activity. Two hundred and one bacterial isolates recovered from peats or from soil taken from the Savannah River Site were co-cultured with *Staphylococcus aureus, Micrococcus luteus,* or *Escherichia coli* on Brain Heart infusion agar to determine which isolates produced a zone of inhibition which is indicative of antibiotic production. In order to identify the genus and species of the antibiotic producing bacteria, the 16s rRNA gene was PCR amplified, cloned and sequenced. The sequences were compared to the 16S rRNA gene database at the National Center for Biotechnology Information. Fifty-seven of the isolates produced a zone of inhibition against at least one of the three test bacteria. Identification of the antibiotic producing bacteria revealed that the main genera were *Bacillus*. The isolates will be retested for against other bacterial pathogens for antibiotic production. In addition, the antibiotics from those isolates that show the greatest activity against the most test bacteria will be purified and their structure determined.

PP155 - Analysis of GerE Binding to the Promoter Regions of *cot* Genes that are Required for Sporulation in *Bacillus subtilis*

Peyton St.John, Dinene Crater

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Bacteria that are placed under environmental stress have the ability to undergo sporulation. One aerobic bacterium that is able to do this is the gram positive *Bacillus subtilis,* which is able to regulate sporulation through transcription control. The DNA binding protein GerE regulates transcription in the later stages of sporulation by interacting with the sigma-K associated RNA polymerase. The focus of our research is to determine if GerE represses transcription of specific genes that are required for the synthesis of the spore coat in *B. subtilis*. We hypothesized that GerE binds to specific sites on promoter regions of *cotA, cotE,* and *cotH*, therefore repressing transcription. To determine if our GerE can bind to the promoter regions, we cloned *gerE* into pET28a and expressed the protein in *Escherichia coli*. Purification using the miniprep protocol under native conditions of the QIAexpressionist kit (Qiagen) gave inconsistent Electrophoretic Mobility Shift Assay (EMSA) results. Therefore, our current focus is to use the QIAexpress Ni-NTA Fast Start kit to purify GerE from *E. coli*. With this new method, we anticipate a higher protein yield and a cleaner preparation, which should affect GerE's ability to bind DNA. We will then use this new preparation of GerE in EMSA reactions to show binding of GerE to the *sigK* promoter as a positive control. Future plans will be to ensure our new purification method enables GerE to bind to GerE-activated promoters such as *cotC* and *cotX,* as well as

showing that GerE can bind to *cotA, cotE,* and *cotH*, allowing the repression of transcription during sporulation.

PP156 - Antimicrobial Properties of Plant Extracts against ESKAPE Pathogens

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Antimicrobial resistance in nosocomial pathogens is a current global health crisis (Simpkin 2017). The pathogens that are the leading cause of nosocomial infections throughout the world are grouped as the ESKAPE pathogens: *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* species (Santajit 2016). ESKAPE pathogens have become increasingly resistant to antibiotics mandating the search for alternative antimicrobial substances. To this end, organic compounds were extracted from 16 different plants with methanol, the methanol was allowed to evaporate, and the extracts were reconstituted with sterile water. These extracts were screened for inhibitory activity against the ESKAPE pathogens by disk diffusion tests. For the extracts that demonstrated inhibition, the method to determine the lowest concentration that would prevent visible growth of bacterium was a microtiter MIC determination assay. The absorbance data of bacterial cultures containing plant extracts at different concentrations was recorded over a 16-hour period. This would demonstrate if there was inhibition on any part of the bacterial growth curves instead of only an end-point determination. Of the plant extracts tested via disk diffusion, six demonstrated inhibition against ESKAPE pathogens: leaf of *Phytolacca americana* (pokeweed), fruit of *Solanum sisymbriifolium* (sticky nightshade), stem and leaves of *Coriandrum sativum* (cilantro), clove of *Allium sativum* (garlic), and leaf of *Laurus nobilis* (bay leaf). In particular, the plant extract from *L. nobilis* inhibited the growth of *S. aureus* and *E. coli* even at diluted concentrations indicating that this extract contained antibacterial properties against both skin and gut bacteria. Other plant extracts also demonstrated inhibitory activity at different titers. These findings indicate potential sources of underutilized antimicrobial agents in plant extracts and the methods outlined in this study could inform future efforts in the search for remedies against antimicrobial-resistant bacterial pathogens.

PP159 - Inhibition of *Elizabethkingia anophelis* biofilm formation and quantification under specific conditions

Elizabeth Florida, William Penwell

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Most bacteria contain the ability to produce a thin, slimy film of cells that adheres to biotic and abiotic surfaces, called a biofilm. The action of biofilm formation plays a significant role in the ability to cause an infectious disease in the host and assists in survival by acting as a protective layer, aiding in resistance against stressors, toxins, and antibiotics. *Elizabethkingia* is a Gram-negative, opportunistic pathogen that is considered an emerging pathogen in the health-care environment. *Elizabethkingia anophelis* is associated with neonatal meningitis and nosocomial outbreaks. This bacterium belongs to the family of Flavobacterium and demonstrates resistance to many different antibiotic classes. Much of the research performed on *E. anophelis* focuses on epidemiology and genetics but there has been a lack of investigation on the basic pathogenesis on this bacterium's formation of biofilm. The goal of this project is to test the various conditions that *E. anophelis* produces biofilm, which include temperature, iron availability, pH, duration of time, and different surface materials (i.e. polystyrene vs. glass). Data from this study will lead to an increase understanding of the pathogenesis of *E. anophelis* and the role of its biofilm in human disease.

PP160 - Effect of seasonality on the prevalence and infection intensity of the fungal pathogen *Batrachochytrium dendrobatidis* in a population of eastern newts

Jubin Kang, Savannah Whitney, Matthew Becker

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Chytridiomycosis, an emerging infectious disease (EID) caused by *Batrachochytrium dendrobatidis* (Bd) contributes to the decline of amphibian populations. Amphibian species show various levels of tolerance to *Bd* infection. *Bd* infects many amphibian populations throughout the eastern United States, yet the population level impact of these pathogens for most species is undetermined. Therefore, this study incorporated a 3-year longitudinal analysis (2017-2019) to evaluate the seasonal prevalence and intensity of Bd infection on the eastern newt (*Notophthalmus viridescens*), a common and widespread species in the eastern United States. The eastern newt is highly susceptible to Bd infections, but the effects of chytridiomycosis on this species is unknown. Approximately 20 eastern newts were collected and sampled quarterly at a pond in Campbell County, Virginia. To sample for Bd, the skin of each newt was swabbed with a sterile rayon swab. DNA was extracted from swabs and amplified via qPCR with Bd specific primers to quantify Bd. The sex, snout-vent length, and mass were recorded for each newt as demographic data. Environmental variables such as air, water temperature, and recent precipitation history were also recorded during each sampling event. Preliminary results show that a high proportion of newts are infected with Bd (Range: 11-100% per quarter) and prevalence of the pathogen varies with season with a greater prevalence in colder months. Once we complete sample collection, infection Bd pathogen dynamics will be compared between three years of quarterly sampling (2017, 2018, and 2019) and correlations with abiotic factors will be identified. Future work will entail monitoring eastern newts to determine if there are any population-level effects of chytridiomycosis.

PP161 - Are *E. coli* resistant to Penicillin and Tetracycline in the Cumberland River in Nashville, TN?

Maria Brauer, Chris Barton, Matthew Heard

Belmont University, Nashville, TN

Humans often release un-metabolized antibiotics into wastewater, which can drain into local waterways via wastewater treatment plant effluent. Repeated exposure to these antibiotics in urban rivers where wastewater effluent is released can subsequently allow bacteria to develop antibiotic resistant properties. In this study, we examined whether bacteria in the Cumberland River in Nashville, TN showed resistance to two common antibiotics, which are frequently found in wastewater effluent – Penicillin and Tetracycline. To answer this question, we collected water samples from eight locations along the Cumberland River in January and February of 2019. At each site, we determine whether water samples were positive for *Escherichia coli*, which is a common fecal indicator bacteria species. When positive samples were found, we isolated *Escherichia coli* colonies and determined how common resistance was to these two antibiotics. Using this approach, we found that 138 of our 160 water samples were positive for *E. coli* and that 136 of these 138 samples were resistant to Penicillin. In contrast, we found that 41 out of 138 samples were resistant to Tetracycline. In addition, we found that there was variation for Tetracycline resistance depending on where the sample was collected. Our findings ultimately suggest that antibiotic resistance poses a threat to the Cumberland River, but that this threat may vary depending on the class and type of antibiotic.

PP162 - Host Range Investigations of Novel Bacteriophages

Bethany Wise

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Bacteriophages are viruses that infect bacterial cells, using them as a host to express their genetic material and replicate. Since phages have the ability to lyse a bacterial cell, it allows the phage to travel to a new host and repeat the process. Some bacteriophages use a specific strain of bacterial host for this procedure, while others have a wider host range, which could be advantageous to the phage under certain conditions. This study aims to help understand this particular area of phage-bacteria interaction by investigating the ability of specific novel bacteriophages to infect and replicate in alternative hosts. To investigate host range, bacteriophages originally isolated from *Microbacterium foliorum* were tested for their ability to infect and lyse *Microbacterium testaceum, Microbacterium paraoxydans, Microbacterium liquefaciens and Mycobacteria smegmatis.* Spot titer assays demonstrated plaque formations on alternative microbacterial hosts by two of the 16 phages (MonChoix and Sirkeiram). Three of the phages (Aries55, BravoCanis and Iann) were able to infect *Mycobacteria smegmatis*. For the next step, two novel phages (Ixel and Nebulous) were isolated from bacterial host *M. liquefaciens*. Using *M. liquefaciens* as the host, the infective ability of Ixel and Nebulous was compared to the infective ability of the *M. foliorum* phages MonChoix and Sirkeiram. The phenotypic measure of infectivity is termed Efficiency of Plating (EOP). For both the *M. liquefaciens* isolated phages, the EOP was less (<1) when compared to the host phages. It is likely that the expression of particular genes in the genomes of phage and bacterial host is able to influence this phenomenon. A number of the phage genomes have been, or are in the process of being, annotated. Comparative analysis of the genomes, and further testing phenotypically, will help elucidate whether specific genes are present that function to enable phage to use a wide host range.

PP163 - Mission Impossible: The Shotgun Cloning and Antibiotic Extraction From A Novel *Zooshikella species*

Aubrey Carey, Magnolia Valdez, Eric Warrick

State College of Florida, Bradenton, FL

Antibiotic resistance has become a prevalent problem in recent decades, as fatalities from previously preventable infections continue to rise. If no significant action is taken by 2050, multidrug resistant bacteria will result in more deaths than cancer and diabetes combined (Small World Initiative). While it is not a matter of "if" bacteria will become resistant to new antibiotics, but "when", we hope to prepare ourselves for the next lethal strain of resistance. Following protocols outlined by the Tiny Earth Initiative, student Danielle Pearman isolated a bacterium, MI3, from North Beach Florida in Fall 2015, which we believe to be a novel species of *Zooshikella* based on previous sequencing results. When initially isolated, the bacteria displayed antimicrobial properties against both Gram-positive and Gram-negative bacteria. The research conducted and shown in this presentation focuses on MI3's antimicrobial activity against *Staphylococcus epidermidis* and further genetic analysis of the genome. An initial chemical extraction in a mid-polar solvent, Ethyl Acetate, was performed using a rotary evaporator. Further extractions were performed using an affinity purification column and an SPE manifold. The column was run using prepared solvent blends varying in polarity from least polar, hexane, to most polar, ethanol. Fractionations were tested for antibacterial activity against *S. epidermidis.* All fractionations showed zones of inhibition except for one solvent blend, 50% Ethyl Acetate and 50% Ethanol. Fractionations were then sent off to our collaborator at Florida State University for LCMS. Returned data provides us with known weights of molecules that could be the antibiotic(s). Further Analysis of MI3's genome was conducted by shotgun analysis, also discussed in this poster.

PP164 - CosmiColi: Engineering highly radioresistant E. coli via tardigrade proteins.

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Investigation into proteins/genotypes which confer radioresistance, as well as their effect on bacterial mutation rate and adaptability, is warranted, due to applications which could include development of a bioremediation chassis for high radiation environments, a means to aid radiation-induced microbiome damage, and as a method to increase genomic stability and decrease evolutionary processes incurred in higher radiation environments. Previous research into the novel tardigrade proteins *damage suppressor* (Dsup) and *cytosolically-abundant heat-soluble protein 94063* (CAHS 94063) have shown increased radiation and desiccation tolerance of transformed E. coli strains.

Via a chromatic Ames Test, we aim to assess the effect of CAHS and Dsup expression on the rate of mutation under UV light exposure, which has not yet been investigated. Additionally, the highly radioresistant strain *E. coli* IR9-50-1 will be transformed with Dsup and CAHS expression systems to assess whether the radiation resistance can be increased via exogenous proteins.

PP165 - Fatty acid-mediated effects on membrane remodeling, virulence phenotypes, and antimicrobial resistance in *Vibrio alginolyticus* and *Vibrio fischeri*

David Smith[1], Ayanna Esdaile[2], Carina Houck[1], Allycia Lee[1], Steven Symes[1], David Giles[1]

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Vibrio alginolyticus and *Vibrio fischeri* are Gram-negative bacteria found globally in marine environments. Studies have shown that certain bacteria (i.e. *Escherichia coli* and *Vibrio cholerae*) are capable of using exogenous polyunsaturated fatty acids (PUFAs) to modify the phospholipids of their membrane. Moreover, exogenous PUFAs have been shown to affect certain phenotypes that are important factors of virulence. The purpose of this study was to investigate whether *V. alginolyticus* and *V. fischeri* are capable of responding to exogenous PUFAs by remodeling their membrane phospholipids and/or altering behaviors associated with virulence. Thin Layer Chromatography (TLC) analyses of extracted phospholipids following exposure to individual PUFAs provided qualitative data supporting fatty acid incorporation. Exogenous fatty acid assimilation was confirmed by Ultra Performance Liquid Chromatography / Mass Spectrometry (UPLC/MS). Several growth phenotypes were identified when individual fatty acids were supplied in minimal media and as sole carbon sources. Interestingly, both linolenic acids inhibited growth of *V. fischeri*. Significant alterations to membrane permeability were observed depending on fatty acid supplemented. Strikingly, arachidonic acid (20:4) reduced membrane permeability by approximately 35% in both *V. alginolyticus* and *V. fischeri*. Biofilm assays indicated that all fatty acids except 18:3

PP166 - Identification of *Vibrio cholerae* Genes Controlling Fatty Acid-Mediated Biofilm Formation in Host and Aquatic Environments

Isabel Gray, David Giles

The University of Tennessee at Chattanooga, Chattanooga, TN

Vibrio cholerae is a gram-negative waterborne pathogen that causes considerable worldwide morbidity and mortality each year. Previous research has shown that *V. cholerae* responds to various fatty acids by altering behavior associated with virulence. Specifically, motility, biofilm formation, and antibiotic resistance were altered depending upon the fatty acid administered. The current study investigated the impact of three exogenous fatty acids on biofilm formation, an important survival, persistence, and pathogenicity trait of bacteria of medical importance. After previously identifying mutants implicated in biofilm development in complex media, we extended our investigation to examine specific environmental conditions (temperature, pH, and salinity) pertinent to *V. cholerae*'s biphasic lifestyle: ocean and human host conditions. As in the first iteration of this study, we subjected the candidate mutants to 3 physiologically relevant fatty acids (linoleic acid [18:2], arachidonic acid [20:4], and docosahexaenoic acid [22:6]). Each mutant's growth characteristics and biofilm formation were assessed under oceanic (30°C, pH 8.1, 600mM NaCl) and human host (37°C, pH 7.1, 150mM NaCl) conditions. As indicated in the preliminary research, temperature and salt induced changes in biofilm formation and growth among the selected mutants. Our results demonstrate an environmental condition-specific response for biofilm formation. Ocean conditions elicit significantly higher biofilm production in the absence of fatty acids. While 22:6 yielded higher biofilm amounts in human conditions, 20:4 generated the most biofilm under ocean conditions. Interestingly, some mutants exhibited divergent biofilm behavior; specifically, the VCA0658 mutant was only able to form biofilm in human conditions when 22:6 was supplemented. The VC1081 and VC1298 mutants displayed higher biofilm formation without fatty acids. Collectively, we have identified intra- and inter-conditional dependencies among *V. cholerae* wild-type and MCP mutants that will further our understanding of fatty acid-mediated biofilm formation.

PP167 - Rate of Infection by Pathogen in Traumatically Injured Patients According to Mechanism and Location of Injury

China Jackson

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The continuous evolution of bacterial pathogens requires rigorous efforts to maintain accurate and current data on hospital-acquired infections in order to better prevent, diagnose, and manage infectious processes. Patients with traumatic injuries are at an increased risk of infection. The interruption in tissue integrity, hemorrhage, hypo-perfusion, and the need for prolonged use of indwelling medical devices impair host defense mechanisms. While the rate of infection in traumatically injured patients has decreased over time, infection rates in this population consistently remain higher than in other ICU populations. A need for further study to determine the prevalence and rate of bacterial pathogens most commonly responsible for these infectious complications is warranted. Data for this study was obtained from patient charts at a level-one trauma center ranging from March of 2016 to March of 2019. Subjects were grouped based on categories of injury followed by location of injury. Patients suffering from immunosuppressive conditions were not included in the study. Preliminary data shows penetrating abdominal injuries to carry the highest rate of pathogenic infections. It is further noted in preliminary data that all injuries regardless of mechanism or location carry a greater risk of infection during the months of May and June. Further in-depth analysis is to be conducted over the following months. The purpose of this study is to identify the rate of infection by pathogen in traumatically injured patients according to type and location of injury. Data collected in this study can be utilized to improve protocols used to screen and treat infectious complications in traumatically injured patients.

PP168 - Flora of Alligator Creek Wildlife Management Area, Wheeler County, Georgia

Richard Carter[1], Frankie Snow[2], Jacob Thompson[3]

[1]Valdosta State University, Valdosta, GA, [2]South Georgia State College, Douglas, GA, [3]Georgia Department of Natural Resources, Brunswick, GA

Recently acquired by Georgia Department of Natural Resources, Alligator Creek WMA comprises about 3,100 acres of sandhills and associated habitats located at the confluence of Little Ocmulgee River and Alligator Creek in the upper coastal plain of southeastern Georgia. Our field efforts since 2017 have resulted in vouchering of 560 vascular plant species, discovery, description, and mapping of populations of 11 rare taxa and description and mapping of more than 15 community types. Rare or otherwise noteworthy plants documented for the area include *Agalinis tenella*, *Elliottia racemosa*, *Litsea aestivalis*, *Marshallia ramosa*, *Penstemon dissectus*, and *Rhynchospora harperi*. Community types include various phases of Xeric Sandhill Forest (from early to relatively intact late successional), Darlington Oak-Mixed Hardwood Upland Forest, Loblolly Pine-Darlington Oak Woodland, Sandhill Swamp Tupelo Hillside Seepage Forest, Loblolly Bay Swamp Forest, Pond Cypress Depression Forest, Maidencane Pond, Slash Pine and Early Successional Flatwoods, Wet Slash Pine-Pond Pine Flatwoods, Early Successional Seepage Swamp, Blackwater Bottomland Hardwood-Pine Forest, and Blackwater Ogeechee Tupelo Floodplain Forest.

PP169 - Inventory, invasive plant removal, and new species discovery at the Webster serpentine outcrop in western North Carolina

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The 12-acre Webster Olivine site in northern Jackson Co., NC, is an outcropping of the large Webster-Addie ultramafic ring. Such outcrops weather into nutrient-poor, heavy-metal rich soils that are unfavorable for the growth of many plants, resulting in savannah-like "barrens" that support rare and endemic species. The Webster outcrop supports a Virginia pine-subtype serpentine community and houses three special status species (*Quercus imbricaria*, *Sporobolus heterolepsis* and *Viola walteri*). Following human disturbance and fire omission, the area is now largely overgrown with weedy species, especially *Smilax* spp. and ragweed, which may be inhibiting the growth of native herbaceous vegetation. In summer and fall of 2018, we conducted a floristic inventory of the site, adding 16 species to a list made in 1994, and established vegetation plots to observe the effects of invasive plant removal on the growth of native herbaceous species. Two 50-m transects were made along a slope across three ecotones (grassland, transitional, forested). Six paired, 2 x 3 m plots were established along each transect, and one plot of each pair was cleared by cutting and one left uncleared. Within each plot, we recorded herbaceous species presence, percent cover, and canopy openness. The experimental plots were recleared of invasive species in 2019, and plots will be resurveyed for new plant growth in 2020. During the inventory, we discovered a likely new species of fleabane similar to *Erigeron strigosus*. Whereas the common fleabane consists of polyploid apomicts, the new species has a diploid chromosome number, like several other recently described, sexually reproducing diploid fleabanes found on various rock outcrop habitats around the southeast. Conservation and habitat restoration on the Webster Olivine site is vital to maintenance of the open, glade-like habitat required by this apparent narrowly endemic species as well as for other rare species specializing on the serpentine outcrop.

PP170 - The Creek Lodge Flora Project

Liam McTigue, Christopher Hardy

Millersville University of Pennsylvania, Millersville, PA

Plant collecting has declined in America over the past few decades. Because specimens are the fundamental records of biodiversity, this decline will have serious consequences in the fields of systematics, land management and education. Thus, a floristic inventory of Millersville University's newly acquired Creek Lodge Property was a necessity. As this 2.05 acre property has great educational potential for use in various biology lab activities, knowledge of its flora is required. This study was concerned with identifying every species of vascular plant on the property by using a point-transect sampling method. A total of 152 unique vascular plant species were identified on the property. Of these 152 species, 124 genera in 58 families, and 33 orders were represented, including several new county records for species previously unknown from the county. Native plants comprised 51.3% (78 spp.) of the flora while exotic plants composed 48.7% (74 spp.) of the flora. An interactive atlas on the Web was also developed to facilitate data management and public accessibility of the findings (Creek Lodge Nature Atlas, http://www.natureatlas.org/plants/creeklodge/). Specimens are vouchered in Millersville University's James C. Park Herbarium (listed as MVSC in Index Herbariorum).

PP171 - A study of vascular plants of the Wingate University Campus Lake and Nature Trail in Wingate, North Carolina

Emily Barbee, Christy Carter

Wingate University, Wingate, NC

Vascular plant diversity at Wingate University's Campus Lake in Wingate, Union Co., North Carolina, was investigated in order to determine plant species presence. Walk-throughs of randomly sampled forested areas, open areas, and nature trails throughout the approximate 4.9 ha site were conducted weekly or biweekly from March through October 2019, and mature specimens were collected for identification. Herbarium specimens stored in the herbarium cabinets of Wingate University, which date back five years collected from this site, were also included in the final species list. Plants collected were photographed in the field and had their GPS coordinates recorded; this information was also recorded into iNaturalist, a website that organized photographic data and enabled a map of species presence to be generated. One to three specimens were collected for each species, placed in bags, and transferred to a plant press. Fresh spec-

imens were used for identification, and dried specimens were reposited at Wingate University. Taxa were primarily keyed using Radford *et al*. (1968), but other keys, including Jones (2005), Weakley (2018), and Wofford (1989), were also used. Nomenclature followed the USDA Plants Database (USDA, NRCS 2020). Keys used were individually cited on herbarium labels. A total of 279 species have been documented, representing a total of 78 families. A total of 270 species represented angiosperms, while 5 represented gymnosperms and 4 represented ferns. No species noted were found to be state or federally listed.

PP172 - Distribution and ecology of the Genus *Asclepias* (Apocynaceae) in Mississippi

Michael Wayne Morris[1], Heather Sullivan[2]

[1]Troy University, Troy, AL, [2]Mississippi Dept. of Wildlife, Fisheries, and Parks, Jackson, MS

Asclepias Linnaeus is a genus of approximately 120 species in the Apocynaceae. This genus is especially diverse across North America, and there are 16 *Asclepias* species occurring in Mississippi: *A. amplexicaulis, A. hirtella, A. humistrata, A. lanceolata, A. longifolia, A. michauxii, A. obovata, A. perennis, A. purpurascens, A. rubra, A. syriaca, A. tuberosa, A. variegata, A. verticillata, A. viridiflora,* and *A. viridis*. The genus as a whole is present in a wide variety of habitats in Mississippi, ranging from coastal savannas and bogs, to xeric fire-prone longleaf pine forests on sandhills, to prairies and interior flatwoods, to alluvial swamp and bottomland hardwood forests, to mesic and dry-mesic hardwood forests and openings on ravine slopes, bluffs, and ridges. Two species, *A. hirtella and A. purpurascens*, are of conservation concern. The additional species *A. humistrata* and *A. rubra* are also monitored by the Mississippi Natural Heritage Program. From November, 2016 through November, 2018, *Asclepias* specimens in the following herbaria were examined at their respective locations: University of Mississippi (MISS), Mississippi State University (MISSA), University of Southern Mississippi (USMS), Delta State University (DSC), Institute for Botanical Exploration (IBE), Mississippi Museum of Natural Science (MMNS), and the Southern Weed Science Laboratory (SWSL). Information on the distribution and habitats of the native Mississippi species will be presented. This research was partially supported by a Troy University Faculty Development Grant, by National Science Foundation grant DBI-1203687, and by the Mississippi Museum of Natural Science Foundation.

PP173 - Distribution and ecology of the Genus *Polygala* (Polygalaceae) in Mississippi.

Michael Wayne Morris[1], Heather Sullivan[2]

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Polygala Linnaeus includes approximately 400 species in the Polygalaceae, and the genus is widespread on a global scale. In Mississippi, 20 *Polygala* species have been recorded: *P. ambigua, P. appendiculata, P. balduinii, P. boykinii, P. brevifolia, P. chapmanii, P. crenata, P. cruciata, P. curtissii, P. cymosa, P. hookeri, P. incarnata, P. leptostachys, P. lutea, P. mariana, P. nana, P. polygama, P. ramosa, P. sanguinea,* and *P. verticillata*. Habitats for the genus as a whole range from swales on coastal barrier islands, to pond cypress depressions, bogs, flatwoods, and pine savannas, to chalk outcrops in prairies, and to sandhills and upland pine-hardwood forests and adjacent clearings and old fields. Four species, *P. appendiculata, P. crenata, P. hookeri,* and *P. leptostachys*, were listed as being of conservation concern in 2018. *Polygala boykinii* was on the watch list in 2018. From November, 2016 through November, 2018, *Polygala* specimens in the following herbaria were examined at their respective locations: University of Mississippi (MISS), Mississippi State University (MISSA), University of Southern Mississippi (USMS), Delta State University (DSC), Institute for Botanical Exploration (IBE), Mississippi Museum of Natural Science (MMNS), and the Southern Weed Science Laboratory (SWSL). Information on the distribution and habitats of *Polygala* species in Mississippi will be presented. This research was partially supported by a Troy University Faculty Development Grant, by National Science Foundation grant DBI-1203687, and by the Mississippi Museum of Natural Science Foundation.

Pp174 - Impacts of Polyploidy on the Ecophysiology of *Solidago altissima*

Katie Krogmeier, Erica Pauer, Howard Neufeld

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The evolutionary importance of polyploidy in plants is still a subject of much research. Polyploidy could be an evolutionary dead end or it could lead to reproductive isolation and creation of new species. Goldenrod (*Solidago altissima*) is a North American herbaceous perennial with diploid, tetraploid, and hexaploid populations: diploids (MWD) and tetraploids are restricted to the midwest while hexaploids occur in both the midwest (MWH) and east (EH). Polyploids generally have larger cells, which can affect stomatal densities, sizes, plant morphology, gas exchange, and plant hydraulics. In a common garden at Appalachian State University, EH had larger and more horizontally oriented leaves than MWD and MWH, but MWH were taller. EH plants had the lowest total chlorophyll amounts. MWD leafed out and flowered earliest, followed by MWH, while EH was the latest. A drought experiment was performed on greenhouse grown plants using a split-pot design. Gas exchange measurements were made using a Li-6800 and water potentials with a Scholander Pressure Chamber. Prior to imposition of drought, photosynthetic rates (A) were higher in MWH and MWD, and lowest in EH. As the experiment persisted through June and July, A and stomatal conductance (g_s) declined in both treatments, but droughted plant rates dropped steeply 7 days after cessation of watering and were significantly lower than those for watered plants. By the end of the experiment, cytotype differences for A and water potential were absent in both treatments. However, g_s remained higher in MWH for watered plants, which also had the lowest water use efficiency among all cytotypes. Light response curves were conducted on well-watered plants and aside from higher light saturated A for MWH plants, no other light response parameters differed among cytotypes. Why diploids do not occur in the east and why MWH and EH differ are currently being investigated.

PP175 - The vascular flora of the Boone Fork Headwaters within Grandfather Mountain State Park, North Carolina

Ethan Hughes

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Grandfather Mountain (GM) is a site of exceptional biological diversity in the Southern Appalachian Mountains of western North Carolina. Long known for its unique assemblage of natural communities and rare and endemic species, GM has been a site of scientific research for many years. GM produces headwater streams for two river drainages: the Watauga and the Catawba River watersheds. The Boone Fork headwaters (BFH) originate on the northeastern slope of Calloway Peak within Grandfather Mountain State Park (GMSP) and represent an area of high natural quality significance. The BFH drain into the Catawba River watershed and represent an area within GMSP for which there is little plant species or natural community data. My project investigated the flora of the BFH and described all vascular plant species and epipetric mosses (rock outcrops and forest boulders) occurring within the roughly 1000-acre study site. Field research revealed 255 vascular plant species, 16 epipetric mosses, and 21 distinct natural communities. Nineteen vascular plant species found during field surveys were categorized as state-listed or federally listed and a few identifications represent new county records. The vascular flora was represented by 77 plant families, ten of which made up over 48% of the species within the BFH.

PP176 - Patterns of Biogeography & Ancestral Ranges in the Scrub Mint Clade (Lamiaceae), Using Target Enrichment for Phylogenetics

Andre Naranjo

University of Florida, Gainesville, FL

The Scrub Mint clade (Lamiaceae) provides a unique system for investigating the evolutionary processes driving diversification in the North American Coastal Plain from both a systematic and biogeographic context. The clade comprises *Dicerandra, Conradina, Pilobleph-is, Stachydeoma, and four species of Clinopodium* (Mentheae; Lamiaceae), almost all of which are endemic to the North American Coastal Plain. Most species of this clade are threatened or endangered and restricted to sand hill vegetation and a mosaic of scrub habitats; some species are restricted to just one or two sites in peninsular Florida and Georgia. Using both novel and established approaches, we analyzed evolutionary relationships in this clade to help us elucidate the biogeography of the group and answer questions regarding ancestral geographic ranges across the phylogeny. We generated a dated phylogeny using a target enrichment/capture dataset. We also estimated the evolution of geographical ranges of subclades and tested whether diversification rates were affected by paleoclimatological events. These results have helped clarify biogeographic patterns in the scrub mints, uncovered potential past diversification events, and helped us better understand past geographic range patterns in the clade.

PP177 - Alabama's Biodiversity Heritage: Expanding and Promoting Access and Use of a Regional Important Botanical Collection.

Michael Woods, Alvin R. Diamond, Anamarie Dahlke, Alyssa K. Webster

Troy University, Troy, AL

In the Fall of 2019, the Troy University Herbarium (TROY) received funding from the National Science Foundation to: 1) acquire a mobile storage compactor system to increase storage space, 2) acquire 72 new cabinets to accommodate growth as well as to replace damaged cabinets, 3) acquire a new camera and macro lens for the imaging of specimens, 4) acquire two computers, two monitors and two external hard drives, 5) employ and train two undergraduate research assistants to assist with the transfer and curation of the collection, 6) process over 10,000 unmounted legacy specimens into the collection, 7) transfer existing herbarium cabinets to the University of West Alabama Herbarium (UWAL), a public institution situated in the impoverished region of Alabama known as the Black Belt, 8) conduct workshops on plant identification and classification for the Alabama Science in Motion (ASIM) program and the Alabama Math, Science, and Technology Initiative (AMSTI), 9) serve as mentors for teachers and students using iNaturalist. These collection improvements will allow for expansion for up to 25 years at the current rate of growth of 2,200 specimens annually.

PP178 - Molecular Phylogeny of the Southeastern Native Species of Wax Myrtles (Genus Morella (Myricaceae))

Sean Eagan[1], Tom Diggs[2]

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The genus *Morella* Loureiro (Myricaceae) consist up to three to five species native to the Southeastern United States, however, approximately 41 exist worldwide. One of these species, *M. pumila*, has questionable identity and has frequently been treated at the varietal rank under *M. cerifera* L.. Weakley (2015) states that these species can live next to each other while remaining distinct. While *M. pumila* has been reportedly collected from different states in the southeast, their identity is uncertain. This project looks to clearly identify *M. pumila* and develop a phylogeny for the eastern species of *Morella* by comparison of the chloroplast trnK/matK intron, and the nuclear ribosomal ITS region. A previous study (Herbert, 2002) looked at the phylogeny of Myricaceae using ITS and trn-L regions. In her study Herbert used three samples that are native to the east coast of the United States, but she did not include varietal taxa. We aim to build upon her work. Starting in the fall of 2019 and continuing into the spring of 2020 DNA extractions on all known Southeastern species (*M. cerifera, M. pumila, M. caroliniensis, M. pensylvanica, M. inodora*) have been performed at the University of North Georgia. PCR amplification began in the Spring of 2020 and sequencing is set to start in the fall of 2020.

PP179 - Quantitative assessment of prevalence and loading of *Labyrinthula* spp. by q-PCR in a tropical seagrass pathosystem

Kylie Harris, Isabelle Zoccolo, Dan Martin, Cliff Ross

Department of Biology, University of North Florida, Jacksonville, FL

Seagrass beds are declining on a global scale due to overexploitation, physical modification of the environment, nutrient and sediment pollution, and the introduction of nonnative species. Seagrass wasting disease is an additional concern that has historically been overlooked. The pathogen responsible for seagrass wasting disease, *Labyrinthula spp.,* is an opportunistic pathogenic protist that has been implicated in the decimation of seagrass beds in many coastal ecosystems. The disease has previously been assessed by quantifying lesion size on infected individuals. However, lesions are not always associated with disease. The objective of this study was to utilize a newly developed q-PCR assay to assess the prevalence and pathogen loading of *Labyrinthula* spp. within turtle grass (*Thalassia testudinum)* tissue collected from five different sites in the Florida Keys in an effort to identify infection severity. Samples were collected from Key West, Marquesas Key, and the Dry Tortugas in 2016 and 2018. There was a high degree of intra- and inter-site variability which may be attributed to site specific factors such as environmental conditions, host genotypes, or host physiological activity. Future work will explore these relationships.

PP180 - Phylogeography of the *Phlox glaberrima/carolina* complex in the southeastern United States

Gerald Bresowar

Emory and Henry College, Emory, VA

Phlox glaberrima L. and *P. carolina* L. have a confusing taxonomic history, complicated by likely hybridization and probable plasticity of diagnostic characters. Here we report on investigation into the phylogeography of the complex across the southeastern United States. Herbarium and field collections were used to construct a chloroplast haplotype network (n = 42, 2 cpDNA regions) suggesting three major haplotype neighborhoods and a potential origin of dispersal in central Alabama. We then sampled nineteen populations over seven states using RAD-sequencing in order to test this hypothesis of origin. We report on these efforts to disentangle the knotty relationships in this complex, and shed light on the morphological and genetic identity of these taxa.

PP181 - Phylogenetic Diversity Patterns as an Aid to Conservation of the Flora of Florida

The importance of plants is often underestimated due to a tendency for inherent “plant blindness”; however, plants provide ecosystem services that humans could not live without. Conserving Earth’s vast diversity of plant species is difficult, especially when funds and time are limited; determining the most beneficial areas to be considered for conservation is crucial. Areas with high levels of phylogenetic diversity or PD, i.e., those areas with diverse evolutionary history and ecological processes, may fare better for directing conservation efforts. Florida has the second longest coastline in the United States; a very large portion of the state is open to impact from hurricanes from either the Gulf of Mexico or the Atlantic Ocean. Mangroves can absorb storm impacts and stabilize land through preventing erosion; unfortunately, mangroves and other crucial vegetation lining the coasts of Florida are sensitive to the effects of sea level rise (SLR), hurricanes, and other impacts of climate change. Increasing anthropogenic factors threaten all ecosystems in Florida; action is needed to protect the diversity of Florida’s coastal flora. Detailed documentation of this flora, both physically and genetically, is important for interpreting and conserving the rich diversity of these coastal plant assemblages. Through sampling natural coastal plant populations, I will obtain sequence data for as many species as possible for inclusion in a phylogenetic tree of the plants of Florida. Phylogenetic diversity will be evaluated spatially across Florida, and areas of high PD will be considered promising areas for plant (and habitat) conservation. These areas will be compared with current protected areas to assess how well PD is currently captured by local, state, and federal protection. With the inclusion of critical coastal taxa, I can then assess areas of high PD, designate areas of high conservation concern, and share my results with governmental agencies and land managers.

PP182 - *Fothergilla* (Hamamelidaceae) reconsidered: A new species and the resurrection of *F. parvifolia*

Jake Haynes, Whitney Phillips, Alexander Krings, Nathan Lynch, Thomas Ranney

North Carolina State University, Raleigh, NC

Fothergilla is a small genus of deciduous shrubs native to the southeastern United States that depending on circumscription comprises two to four species. Recent treatments recognized only two species in the genus: *F. gardenii* (tetraploid) and *F. major* (hexaploid). Until recently, no diploid taxon of *Fothergilla* was known. However, recent investigations identified a number of diploid populations in the Southeast. A subsequent phylogenomic analysis showed that the diploids segregated into two, well-supported lineages, corresponding to largely allopatric populations. A re-examination of the morphology of diploid plants, in combination with the genetic evidence, led us to the recognition of two species of diploids in the genus—a resurrected *F. parvifolia* and a new species—bringing the total number of recognized species in *Fothergilla* to four.

PP183 - Effects of bisphenol-A on nerve activity in *Lumbricus terrestris* and *Procambarus clarkii*

Destiny Sciuva, Todd Wood, Abby Kruger, Julie Wilson, Madison Chen, Claud Bugheni, Jaleesa DeJesus, Meenal Joshi, Erin Perry, Justin Rush, Skylar Smith, Jordan Spires, Nicholas Wilson, Kathleen Hughes

Columbus State University, Columbus, GA

Bisphenol A (BPA) is a widely used plasticizer that has gained controversy in recent decades due to increasing concern of biological and ecological disruption. Research has shown that BPA produces a wide variety of adverse effects on processes related to development,

metabolism, and general survival. Scientific findings on the effects of BPA as an environmental contaminant are fragmented in regards to regulatory implications and overall ecosystem disturbance. Previous studies show measurable harm from BPA exposure in organisms at environmentally-relevant concentrations defined at equal to or less than 12 µg/L. For the purposes of this study, we exposed both an aquatic and a terrestrial invertebrate to 10 µg/L BPA to determine the effects on key features in nerve activity in separate trials. Results displayed a statistically significant decrease in both frequency and amplitude of nerve activity across all treatments at increasing voltage levels along with other morphological changes in the common earthworm, *Lumbricus terrestris* (2-way ANOVA, $F36,324=32.18$, $P<0.0001$). For the crayfish, *Procambarus clarkii*, there was no significant difference between control and BPA groups in regards to frequency and/or amplitude of action potential, but there was significance from the mean, showing progression toward potential change if more trials were tested. The results of this study indicate that BPA does have an effect on nerve activity in the invertebrates tested. Further studies on the effect of such toxicants can provide recommendations for updated and more frequent environmental contaminant testing for better regulatory and conservatory management.

PP184 - The Effect of Hand Dominance on Nerve Conduction

Kasandra Myers, Heather Evans Anderson, Michele Skelton

Stetson University, Deland, FL

There is limited research on how hand dominance relates to the speed of nerve conduction. Research on the relationship between handedness and nerve function may be beneficial in rehabilitation of cerebrovascular accident patients. In stroke patients, loss of strength and mobility occurs when nerve function decreases. Stimulation of sensory nerves in stroke patients promotes recovery and handedness may be an important consideration in treatment plans. Hand dominance occurs due to persistent overuse of one hand, which creates stronger neural pathways in comparison to the non-dominant side. The purpose of this study was to determine if differences in nerve conduction strength could be measured between dominant and nondominant hands in healthy subjects in order to establish a baseline to which measurements from stroke patients could be compared. Twenty-four, college-aged males and females were recruited for this study. An iWORX 214 lab kit was used to measure nerve conduction velocity by administering median nerve stimulation through electrodes. Electrodes were placed in 5 locations on the hand and lower arm. Stimulation began at 0.0 volts, then increased 0.5 volts up to a maximum stimulation of 1.5 volts in order to measure the amplitude of muscle response. Labscribe 4 Data acquisition and Analysis software was used to collect data. A paired samples t-test compared data from dominant to nondominant hands. Dominant hand nerve conduction velocity was 0.0029 volts ± 0.0014 and non-dominant hand nerve conduction velocity was 0.0023 volts ± 0.0012. Preliminary results showed a statistical significance ($p \leq 0.05$) between dominant and non-dominant hands. Further research will include measurement of both motor and median nerve conduction velocity.

PP185 - Difference In Physiological Responses to Excitatory Sound Stimulation in Humans Subjects

Ansley Glenn, Joni Criswell

Anderson University, Anderson, SC

Sound can act as an intrinsic warning system and a soothing source in individuals. Sounds can often affect mood, such as decreasing anxiety, bringing pleasure, or joy. However, the excitatory effects of sound on human physiology have not been thoroughly studied. Here, we examined the heart rate, blood pressure, and brain responses to excitatory sounds to determine their effects on individuals.

PP186 - Skeletal Pathologies in Carnivores (Mammalia, Carnivora): A Systematic Overview of Prevalence Based on an Analysis of Museum Specimens

George Argyros

Emory and Henry College, Emory, VA

Museum specimens representing 117 species of terrestrial and aquatic/marine carnivores (Mammalia, Carnivora) from 11 families were inspected for evidence of traumatic and congenital skeletal pathologies. Of 829 individuals evaluated, 109 (13%) exhibited some form of skeletal abnormality. Observed conditions were categorized as either healed fractures, variations of osteoarthritis (OA), or non-specific osteopathologies. Of the 109 individuals, 65 (60%) exhibited healed fractures; primarily of the long-bones. Osteoarthritis of appendicular joints and in the axial skeleton resulting in osteophytic or enthesophytic growths was observed in 48 individuals (44%). Ankylosing Spondylitis (Spondyloarthropathy) was evident in the majority of individuals where OA was present in the vertebral column. Diffuse Idiopathic Skeletal Hyperostosis (DISH) was also observed in at least five individuals, the majority (3 of 5) occurring in the Pinnipedia. Specimens representing the Canidae had the highest number of observed healed fractures (32%). Little is known regarding the prevalence of these types of skeletal pathologies in wild mammalian carnivores, and even less is known as to causation. Given that the evidence of such injury, or degenerative nature of arthritis is not generally observable in the wild antemortem, and is primarily only evident upon necropsy and subsequent skeletal preparation for museum collections, more studies need to be executed on living specimens to evaluate the impacts of such injuries/pathologic conditions on behavior and survival in the field.

PP187 - Analysis of the Neuromuscular Junction with Fluorescent Microscopy

Hannah Forrest, Jordan Paine, Jessica Nicks, Joni Criswell

Anderson University, Anderson, SC

In this project, we set out to determine whether or not there were any visible differences in integrity between specific muscle groups of different cadavers through analysis of their neuromuscular junctions. We compared cadavers that died of age-related complications versus those that suffered from a disease or other complication and determined whether or not differences in their neuromuscular junctions and/

or muscle integrity are present. We specifically compared three cadavers, who suffered from chronic alcohol abuse, cerebral palsy, and eventually died from age-related complications, respectively. We hypothesized that muscle integrity would be most negatively affected in the cadaver that suffered from cerebral palsy and that this would be observed in the reduced number of neuromuscular junctions visible after antibody treatment and examination under the fluorescent microscope. We concluded that based on the amount of positive staining that showed after treatment, the cadaver that suffered from cerebral palsy and the cadaver that suffered from age-related complications had the same amount of neuromuscular junctions visible, whereas the cadaver that suffered from chronic alcohol abuse had the least amount of junctions visible.

PP188 - Lipid Induced-EV Proteins and their Association to Diabetic Kidney Disease

Amanda Haney[1], Alyssa Cobbs[2], Xueying Zhao[2]

[1]Georgia Gwinnett College, Lawrenceville, GA, [2]Morehouse School of Medicine, Atlanta, GA

Abnormal lipid metabolism in association with type 2 diabetes, plays a major role in the development of diabetic kidney disease (DKD). Lipotoxicity, an accumulation of intracellular lipid metabolites, has been proposed as a mechanism which mediates renal tubulointerstitial damage. Extracellular vesicles (EVs) are cell secreted molecules that are believed to be vital in mediating intracellular communication and immune regulation. Our lab investigated the effect of fatty acids on EVs released from cultured renal proximal tubular cells (PTCs). NRK-52E cells were treated with palmitic acid (PA) and 1% BSA. Secreted EVs were isolated through ultracentrifugation and proteins were identified using liquid chromatography, electrospray mass spectrometry (LC-ESI-MS/MS). Our results indicate PA dose-dependently increases EV production. Additionally, protein pathways with known DKD associations were identified from EVs via the Metacore Analysis Program and literature search. Furthermore, the novel pathways and mechanisms discussed can serve as rationale to further evaluate PA-induced apoptosis and injury in renal tubular cells.

PP189 - *A Paleohistological Investigation into the Caudal Vertebral Anomalies Observed in Some Mosasaurids (Reptilia: Squamata)*

Sahara Gonzalez[1], Michael Burns[1], Jun Ebersole[2]

[1]Jacksonville State University, Jacksonville, AL, [2]McWane Science Center, Birmingham, AL

Mosasaurs were squamates that filled a marine apex predator niche during the Late Cretaceous period. A survey of mosasaur fossils collected in Alabama over the years has identified at least 1,300 specimens. Among marine reptiles, mosasaurs appear to exhibit an unusually high instance of anomalies indicating caudal vertebral fusion or lack of segmentation; a condition that has been directly examined across several genera including *Platecarpus*, *Clidastes*, and *Tylosaurus*. Little research has investigated the etiology of these abnormalities. In this study, we test three hypotheses to explain this cause; normal development, pathology, or healed injury.

Several specimens exhibiting caudal fusion or lack of segmentation, collected from the Upper Cretaceous Mooreville Chalk, were used for paleohistological analysis. Before sectioning, specimens were molded and casted to preserve morphological data, and stabilized by resin impregnation. The sections were then prepared petrographically on frosted Plexiglass slides. Our analysis indicates no *in vivo* fusion in two of the specimens, whereas, one does display an anomaly.

The unfused specimens show trabecular bone in the medullary regions of the vertebrae; however, towards the cortex, in particular, the anterior and posterior margins, the bone tissue becomes denser. This histology is typical for vertebrae. In the fused specimen, the trabecular bone density is constant throughout, with no indication of an intervertebral disk, calcified cartilage, or woven bone. Because the trabecular bone density is constant and no evidence of woven bone (indicative of injury or a pathology) can be observed, evidence supports the hypothesis that this anomaly is indicative of normal bone development. However, it is important to note that, if this anomaly was due to pathology or breakage, remodeling could have erased such a record. Therefore, although the histological evidence indicates a developmental process normal for these taxa, the alternatives cannot be completely ruled out without further study.

PP190 - Behavioral impact of the flavorant cinnamaldehyde on adult zebrafish

Cory Weller, Eric Bauer

Elon University, Elon, NC

Humans consume a myriad of chemicals daily, via ingestion, dermally, or inhaling. For most of these chemicals, we have little idea as to what they may be doing to our body. Additionally, even if one chemical is shown to be safe to consume in one modality, i.e. eating, this does not guarantee that the same chemical will be safe to consume through another modality, i.e. inhalation. This is a common situation in vaping solutions which use flavorants approved for ingestion but in the novel modality of inhalation. It is entirely possible that how a molecule enters the blood stream and interacts with the body will differ between the digestive and respiratory systems. Our research uses behavioral assays of swimming and neophobia in zebrafish (*Danio rerio*) to look for potential neurological impacts of vaping flavorants. Neophobia (fear of novelty) is a complex task and requires engaging several high-level cognitive processes (visual processing, object recognition, and memory formation and recall) which lead to alteration of behavioral output by the animal. Even minor disruptions by a chemical of neurological functions will manifest as differential behavioral choices as compared to control animals. Zebrafish are an acceptable model to study the potential behavioral impacts of e-cigarettes on humans due to physiological evolutionary conservation in the vertebrate lineage. We test fish before one week of chemical treatment, immediately following treatment, and then 1-week post-treatment. Preliminary results using the flavorant cinnamaldehyde have shown that treated zebrafish swim 30% further and with 29% faster swimming bursts than control fish. This effect persists at least 1 week post-treatment. In addition, cinnamaldehyde-treated fish react with slightly greater fear to changes in their environment. By analyzing general activity and the response to novel objects and environments, the effects of various chemicals on the neurological functions of zebrafish will be studied.

PP191 - Impact of Digitizing Acoustic Waves on Scientific Research: a Case Study

Doris Cruz, Francisco Coro

Miami Dade College, Padrón Campus, Miami, FL

One of the technological advances that has a tremendous impact on many aspects of our everyday life is the digitizing of acoustic waves, as voice recordings. For many decades, starting at the 1920's, the only possibility was to use analog techniques and magnetic recording of these mechanical waves. This implied limitations in the analysis of the information they contained, particularly with ultrasonic frequencies (above 20 kHz), as those emitted by many moth species. Sanderford and Conner (1990), using analog techniques and magnetic recording, described the acoustic emissions of *Syntomeida epilais*, commonly known as the polka-dot wasp moth. These authors were the first to demonstrate the need of acoustic communication during courtship behavior in a moth species with two-celled ears. They also suggested certain features of these emissions that show sexual dimorphism, but were unable to demonstrate them due to technical limitations. During my summer research internship I was able to process and analyze the digitized acoustic emissions from this moth species, using the software BatSound. From these digitized recordings, we have been able to describe previously unknown features of their acoustic signals, as sexual dimorphism in the fine temporal pattern of their emissions. We also showed previously unknown auditory discrimination abilities of females: they are able to discriminate between normal and transformed male signals, responding better to male normal emissions. Our results suggest that this is the "simplest" (or least complex) auditory system in Nature with adaptations for intraspecific acoustic communication.

PP192 - Observational study of behavioral activity patterns in captive *Cuora galbinifrons, Cuora bourreti,* & *Cuora picturata* over time

Mandi Moxie

Queens University of Charlotte, Charlotte, NC

Asian turtle species have been in decline due to multiple anthropogenic pressures. Among the turtles affected are the closely related species; *Cuora galbinifrons, Cuora bourreti,* and *Cuora pitcurata.* Previous research indicates that these species differ in morphology, mitochondrial DNA, and osteology, however their behavior patterns have not been studied. In this study we quantified activity patterns to compare species and sex differences. We found that there were differences in the proportion of time spent performing in male *C. bourreti* when compared to female *C. bourreti*. However, there was no significant difference in active behaviors between species. The findings on sex biased differences in activity levels are similar to other research in different turtle species that examine male dispersal and movement patterns. The similarities in activity patterns between species may be related to their shared ancestry and similar environments. Future studies of the behavior of these species would benefit from larger sample sizes and more consistent patterns of enclosure inhabitants. Additionally, extending the length of behavioral observations would allow for an examination of seasonal differences in behavior.

PP193 - An Auditory System with Two-Celled Ears Discriminates between Mate and Predator

Nila Lumpuy, Francisco Coro

Miami Dade College, Padrón Campus, Miami, FL

Noctuid and erebid moths with two-celled ears that evade their predators, insectivorous bats, have been extensively studied. Among the erebids, some Arctiinae also have acoustic emission organs. *Syntomeida epilais* is one of the few Arctiinae needing acoustic communication for successful courtship behavior. They emit sexually dimorphic acoustic signals, named modulation cycles (MC): males emit them at a lower repetition rate than females. Sanderford and Conner (1995) proposed that *S. epilais* females respond preferentially to their male signals based on their slower repetition rate. Our aim was to test this suggestion by exposing 17 virgin, perched, unrestrained females during their courtship hours to playback of two acoustic series with the same repetition rate (9.2 stimuli.s^{-1}): one with six male MC and the other with six bat search pulses. Each of these stimulation series were applied three times at each of the acoustic intensities used, between 56 and 92 dB SPL. We counted the number of MC emitted by the female to each of these stimulation series. Stimulation series with female response differ significantly: mean to male series 94.7 (SD: 6.2)% and to bat series 51.0 (SD: 30.8)% (Wilcoxon test, $p<10^{-4}$). These and other data demonstrate that *S. epilais* females are able to discriminate between these two series based on the different temporal structure of their acoustic stimuli. These results differ from those described in a noctuid moth in which females are not able to discriminate between the acoustic emissions from conspecific males and those of bat echolocation calls.

PP194 - Interspecific Cooperation of *Philomycus* Slugs and Green Salamanders, *Aneides aeneus*, may enhance water economy

Paul Cupp

Eastern Kentucky University, Richmond, KY

Philomycus slugs and green salamanders, *Aneides aeneus,* are commonly found in the same rock crevices in sandstone rock cliffs. Previous studies suggested that any interactions of *A. aeneus* with slugs in crevices likely were not beneficial for either species. Also, the presence of slugs in *A. aeneus* breeding crevices may be harmful to the eggs. However, I have observed twelve instances in which *A. aeneus* (adults and young) were in direct contact with single *Philomycus* slugs in rock crevices with no apparent ill effects. This water-conserving posture may reduce the surface area exposed by the two animals such that water loss would be minimized and may allow survival over short dry periods until humidity or moisture levels increase. In some cases, additional water conserving measures were observed, including pressing of the tail against the side of the body and coiling it over the head. Both species have a moist integument and thus are readily subject to evaporative water loss. While opportunistic, this aggregative behavior by both species may be adaptive and beneficial. One possible negative effect was in the case of a large slug present in a small *A. aeneus* brooding crevice which may have prevented

deposition of her eggs. The aggregative behavior observed here indicates that interspecific cooperation or mutualistic symbiosis with regard to water economy may be important for some individual slugs and salamanders.

PP195 - Female Moths with an Auditory System with Two-Celled Ears Discriminate between Mate and Predator

Nila Lumpuy, Doris Cruz, Francisco Coro

Miami Dade College, Padrón Campus, Miami, FL

Noctuid and erebid moths with auditory systems with two-celled ears that evade their predators, insectivorous bats, have been extensively studied. Among the erebids, some Arctiinae also have acoustic emission organs. *Syntomeida epilais* is one of the few Arctiinae needing acoustic communication for successful courtship behavior. They emit sexually dimorphic acoustic signals, named modulation cycles (MC): males emit them at a lower repetition rate than females. Sanderford and Conner (1995) proposed that *S. epilais* females respond preferentially to their male signals based on their slower repetition rate. Our aim was to test this suggestion by exposing 17 virgin, perched, unrestrained females during their courtship hours to playback of two acoustic series with the same repetition rate (9.2 stimuli.s^{-1}): one with six male MC and the other with six bat search pulses. Each of these stimulation series were applied three times at each of the acoustic intensities used, between 56 and 92 dB SPL. We counted the number of MC emitted by the female to each of these stimulation series. Stimulation series with female response differ significantly: mean to male series 94.7 (SD: 6.2)% and to bat series 51.0 (SD: 30.8)% (Wilcoxon test, $p<10^{-4}$). These and other data demonstrate that *S. epilais* females are able to discriminate between these two series based on the different temporal structure of their acoustic stimuli. These results differ from those described in a noctuid moth in which females are not able to discriminate between the acoustic emissions from conspecific males and those of bat echolocation calls.

PP196 - The behavioral ecology of the Central American river turtle (*Dermatemys mawii*) in captivity.

Anthony Dunkelberger

University of North Florida, Jacksonville, FL

The critically endangered Central American river turtle (*Dermatemys mawii*), also known as the hicatee, is a large, highly aquatic, freshwater turtle found in Mexico, Belize, and Guatemala. Behavioral ecology of *D. mawii* is unknown and would benefit conservation projects that aim to breed individuals in captivity. The purpose of our study was to create a preliminary ethogram as well as a transition matrix for *D. mawii* in captivity. Over the course of 12 months *D. mawaii* (n=3, 1 male, 2 female) were observed using a focal approach for one hour windows multiple times a week at the Jacksonville zoo. *Dermatemys mawaii* were housed in an aquatic enclosure resembling a pond that allowed clear viewing of behaviors. The enclosure consisted of two other species of Testudines, one species of Osteichthyes, and fourteen species of Aves. *Dermtemys mawii* had low diurnal active states and spent 95% of time resting on the bottom of the pond. The male in our study displayed aggressive behavior such as biting and chasing towards conspecifics but generally ignored other species within the exhibit enclosure. Our findings also revealed previously undocumented behaviors for this species in captivity. A gravid female deposited her eggs underwater at the bottom of the enclosure's pond, presumably due to insufficient variety of nesting grounds within the enclosure. Another female demonstrated an unusual "basking-like" behavior prior to health complications that ultimately resulted in her passing. These findings can be applied to conservation management as one of the main strategies for long-term conservation in captive breeding of individuals for release into wild protected areas. For example, density of males in captivity should be low to reduce aggression and a variety of nesting habitat should be available to gravid females. Surface behaviors, such as basking, should be closely monitored and may indicate stress and/or health issues.

PP197 - Behavioral ecology of the Central American river turtle (*Dermatemys mawii*) in captivity.

The critically endangered Central American river turtle (*Dermatemys mawii*), also known as the hicatee, is a large, highly aquatic, freshwater turtle found in Mexico, Belize, and Guatemala. Behavioral ecology of *D. mawii* is unknown and would benefit conservation projects that aim to breed individuals in captivity. The purpose of our study was to create a preliminary ethogram as well as a transition matrix for *D. mawii* in captivity. Over the course of 12 months *D. mawaii* (n=3, 1 male, 2 female) were observed using a focal approach for one hour windows multiple times a week at the Jacksonville zoo. *Dermatemys mawaii* were housed in an aquatic enclosure resembling a pond that allowed clear viewing of behaviors. The enclosure consisted of two other species of Testudines, one species of Osteichthyes, and fourteen species of Aves. *Dermtemys mawii* had low diurnal active states and spent 95% of time resting on the bottom of the pond. The male in our study displayed aggressive behavior such as biting and chasing towards conspecifics but generally ignored other species within the exhibit enclosure. Our findings also revealed previously undocumented behaviors for this species in captivity. A gravid female deposited her eggs underwater at the bottom of the enclosure's pond, presumably due to insufficient variety of nesting grounds within the enclosure. Another female demonstrated an unusual "basking-like" behavior prior to health complications that ultimately resulted in her passing. These findings can be applied to conservation management as one of the main strategies for long-term conservation in captive breeding of individuals for release into wild protected areas. For example, density of males in captivity should be low to reduce aggression and a variety of nesting habitat should be available to gravid females. Surface behaviors, such as basking, should be closely monitored and may indicate stress and/or health issues.

PP198 - Feeder Cams and Photoperiods: Observing Feeder Bird Response to Sunrise and Sunset

Lauren Pharr, Caren Cooper, Bailey Rayfield, Isaac Carbajal, Holly Keepers, Kelsey Neilan, Leanna Jensen

North Carolina State University, Raleigh, NC

With expanding urbanization, anthropogenic noise and light pollution are having a drastic impact on species activity, communication, and physiology. Specifically, with avian species, circadian rhythms are just one of the many components affected. Thus, the timing of daily activity at bird feeders may vary across a rural or urban environment as well as with other environmental factors such as weather

and photoperiod. We observed three bird feeders via webcams that were located in Recke, Germany, Ithaca, New York, and El Valle de Anton, Panama. At each feeder, we analyzed the frequency and daily timing of bird visits during periods surrounding sunrise and sunset.

By dividing the number of pre-sunrise or post-sunset visits by the total number of visits at dawn and dusk, respectively, we found that about 5.3-6.8% of birds were actively foraging prior to sunrise in all 3 sites while 7.3-12.3% of birds were actively foraging after sunset at all 3 sites. Birds in Germany continued to forage beyond 30-minutes after sunset while birds in New York and Panama stopped foraging within 15 minutes of sunset. During the sampling period, day lengths were longer (~16 hours) in the Northeastern United States and Germany whereas in Panama, day lengths were shorter (~11 hours). Also, during the sampling period, ambient temperatures were lower in the US and Germany (~7.8 degrees celsius and ~8.1 degrees celsius) than in Panama (~24.6 degrees celsius). Environmental conditions may have created different energetic constraints on birds at each site, yet the higher frequency of bird visits in Germany may be due to the lack of mammal competitors at that site.

PP199 - Importance of Eastern Hemlock In Acadian Flycatcher Home Range Use

Jasmine Kelly[1], David Brown[2]

[1]University of North Carolina at Pembroke, Pembroke, NC, [2]Eastern Kentucky University, Richmond, KY

Invasive species play an important role in disturbing ecosystems and causing problems for native species. The invasive Hemlock Woolly Adelgid (*Adelges tsugae*) feeds on starches from needles of Eastern Hemlock (*Tsuga canadensis*). Many bird species rely upon Eastern Hemlock for nesting and as foraging substrate, in part due to retention of understory branches. One of the bird species that preferentially select Eastern Hemlocks is a neotropical migrant, the Acadian Flycatcher (*Empidonax virescens*). Working in southeastern Kentucky, we examined how important Eastern Hemlocks were in Acadian Flycatcher home range use by measuring the extent of their home ranges, recording behavioral observations, and measuring use of Eastern Hemlocks. Vigor of Eastern Hemlock was assessed on a scale of 1-5, with 1 being healthy and 5 being dead. We observed thirteen birds, with sufficient observations to conduct home range analysis (21 ± 8.76 locations per bird). Data were collected using ArcGIS Online to record perching and foraging locations. We then used Geospatial Modeling Environment to conduct a kernel density analysis. Program R was used to run t-tests and create boxplots to compare home range characteristics and behaviors based on the presence or absence of Eastern Hemlock in Acadian Flycatcher home ranges. The results of this study suggests that the presence or absence of Eastern Hemlock did not affect Acadian Flycatchers home range use or behaviors. Also, many Eastern Hemlocks in the home ranges had vigor rankings of 4 or 5 suggesting that the HWA is changing the composition of the forest and other tree species are becoming more dominant. American Beech, Sugar Maple, and Red Maple were commonly used for perching by Acadian Flycatchers and these species will likely become more dominant with the decline of Eastern Hemlock.

PP200 - Synchronous Air Breathing as a Response to Hypoxia Exposure in Two Size Classes of Juvenile Armored Catfish, *Pterygoplichthys disjunctivus*.

Abigail Crater, Melissa Gibbs

Stetson University, Deland, FL

Armored catfish (*Pterygoplichthys disjunctivus*) are invasive to Blue Spring in Volusia County, Florida, a crystal-clear, hypoxic, first magnitude spring. Smaller juvenile armored catfish are rarely found in the spring run, and our main question was "why?". We have observed adult armored catfish swimming to the surface to breathe air under hypoxic conditions, and so we hypothesized that the smaller juvenile armored catfish are not found in the spring run because they are more sensitive to hypoxia than larger individuals, and thus would be more vulnerable to predation when they surfaced for air. To test our hypothesis, we observed two size classes (small (average size = 7 cm SL) and medium (average size = 16 cm SL)) of juvenile armored catfish in varying dissolved oxygen (DO) levels (hypoxia (0-3 mg O_2/L), transitional (3-6 mg O_2/L), and normoxia (>6 mg O_2/L)). We tallied the number of air-breaths per minute and measured the degree of group air breathing (synchronicity) by calculating a coefficient of dispersion (CD) for each trial. Only the smaller juvenile armored catfish exhibited CDs significantly above one ($p < 0.05$), indicating significant temporal clumping of air breathing behavior. Interestingly, the level of synchronicity decreased as the DO levels increased ($R^2 = 0.8736$). Medium juvenile CDs averaged significantly below one no matter the dissolved oxygen ($p < 0.05$), indicating a uniform air-breathing pattern (no synchronicity). There was also no significant change in medium juvenile temporal air-breathing behavior as DO increased ($R^2 = 0.4997$). These results illustrate that smaller juvenile armored catfish are more affected and behave differently in hypoxic environments than larger juvenile armored catfish.

PP201 - Testing predictions of host monopolization theory in the amphipod *Leucothoe tunica* White, 2019 and its ascidian host *Styela plicata* Lesuer, 1824.

Louis J. Ambrosio[1], Kristine N. White[2], Samuel Dixon[1]

[1]University of Tampa, Tampa, FL, [2]Georgia College & State University, Milledgeville, GA

Host monopolization theory predicts that symbiont guests of morphologically simple, small, and scarce hosts increase monopolization behaviors, leading to a solitary lifestyle for symbionts. We tested this prediction with the recently described endosymbiotic amphipod *Leucothoe tunica* White, 2019 and its morphologically simple, small, and somewhat scarce ascidian host *Styela plicata* Lesuer, 1824. *Styela plicata* was collected while snorkeling jetties adjacent to the Sunshine Skyway Bridge in Tampa Bay, Florida from 2016 to 2020. The observed population distribution of *L. tunica* in host ascidians was compared with an expected random Poisson distribution and significant differences between these distributions were determined using a Chi-square test of goodness-of-fit. Counter to our expectations, *L. tunica* was found to inhabit *S. plicata* in large groups more often than expected by chance alone but rarely overlapped with competing endosymbionts like the ascidian pea crab *Tunicotheres moseri* (Rathbun, 1918). While not confirmed, this study suggests inclusive fitness benefits for individuals living in family groups may outweigh individual fitness benefits for *L. tunica* even under conditions of limited host resources. Furthermore, predictions of host monopolization behaviors or avoidance strategies may explain rarely observed cohabitation of heterospecific endosymbionts in host ascidians.

PP202 - Spectral Properties of the Harmonics of the Low Chip Call of the Chinese Blue-breasted Quail Chick (*Coturnix chinensis*).

Edward Mills

Wingate University, Wingate, NC

The low chip call produced by hatchling Chinese Blue-breasted Quail (*Coturnix chinensis*) consists of a short (0.08 sec), low frequency (2908.23 Hz), one-syllable chip that contains two harmonics above (6002.78 Hz, 14572.73 Hz). This low amplitude call (82.9 dB) and its harmonics (60.49, 51.59 dB) likely serve as contact signals between chicks and their parents. These vocalizations deteriorate over active space to help communicate distance and to reduce the interest and focus of predators. The low chip call has not been recorded in adult birds. Individual hatchling chicks were removed from a warming brooder at the age of eight days and placed into isolation for a period of five to ten minutes, and their vocalizations were recorded. Seven spectral properties of the low chip call harmonics were measured: call length (sec), call frequencies (low, high, center, width, Hz), average power (dB) and maximum power (dB). The results indicate that both of the harmonics of the low chip call are produced at a significantly lower amplitude in average power and maximum power (dB) than the harmonics of the 2-syllable B call. The 2-syllable B call is another contact signal produced by quail chicks. In addition, both the average power and maximum power of the low chip harmonics decrease significantly as the signal increases in frequency, so the upper harmonic degrades at a faster rate than the lower harmonic. Because of their low amplitudes (aka whispered), these chick harmonics are likely used by hatchling quail chicks to maintain contact with family members without attracting the attention of predators. It has been shown that low amplitude harmonics degrade over distance to allow a hatchling to convey its location to family members.

PP203 - Investigation of nicotine's ability to mitigate neuroinflammation using a zebrafish model

Gabriella Tyler, Ernest Ricks, Robert Haining, Cindy Achat-Mendes

Georgia Gwinnett College, Lawrenceville, GA

Parkinson's disease is a progressive neurodegenerative disorder originating in the substantia nigra and resulting in the loss of dopaminergic neurons and subsequent dopamine release. This interruption of dopamine is accompanied by inflammation and appears to provide an explanation for the loss of motor function in those who have Parkinson's disease (PD). Reports from the American Academy of Neurology suggest that people who smoke cigarettes are ~44% less likely to develop PD, compared to those who have never smoked. Additionally, nicotine has been shown to activate anti-inflammatory signaling pathways *in vitro*. The goal of this study was to investigate the potential for nicotine to protect against neuroinflammation and loss of motor function. 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP) is a prodrug to MPP+, a known dopaminergic neurotoxin upon exposure. MPTP induces Parkinsonian-like symptoms at specific doses in zebrafish. Thus a zebrafish model was established to investigate the effects of nicotine (5mg/l, 7mg/l) pretreatment on MPTP-induced locomotor impairments and changes in the expression of neuroinflammatory markers in zebrafish. Behavioral analyses was conducted using Ethovision and gene expression was investigated by qPCR. In experiment 1, treatment with MPTP (0.1 ug/ml) for 14 consecutive days increased immobility measures in zebrafish by 350%, compared to the behavior of control fish not exposed to MPTP. In experiment 2, pretreatment with nicotine for 96 hours prior to the introduction of MPTP for 14 days, resulted in significantly less locomotor impairments compared to controls treated with MPTP only. These findings that nicotine can attenuate MPTP-induced mobility impairments, likely through loss of dopaminergic function, along with the discovery of nicotine-induced changes in neuroinflammatory genes e.g. interleukin 6, GFAP, tumor necrosis factor, can help elucidate nicotine's putative role in mitigating inflammation associated with PD.

PP204 - Drug Repurposing: Anti-malarial compounds decrease the viability of multiple cervical cancer cell lines

Hannah Moore, Chris Barton

Belmont University, Nashville, TN

Drug repurposing is the act of using current FDA-approved medications for the treatment of different pathological conditions. Previous research has shown that a number of repurposed drugs are effective at preventing the growth of cancer cells, and some of these molecules are currently being studied in clinical cancer trials. Our laboratory previously found that amodiaquine, a drug typically used for the treatment of malaria, is effective at stopping the growth of cancer cells in culture. Whether other anti-malarial compounds are effective at preventing cancer growth has yet to be determined. Here, we show that to additional anti-malarial drugs, piperaquine and tafenoquine, are both effective at blocking the growth of multiple cancer cell types. We also show that tafenoquine is highly effective at reducing cancer cell viability with an LD50 concentration that is lower than both piperaquine and amodiaquine. Further studies are necessary to determine the mechanism behind the efficacy of these molecules.

PP205 - Transcriptome analysis of the metathoracic scent glands of *Leptoglossus zonatus* (Hemiptera: Coreidae)

Daniel Burckhalter, David M. Donnell

The Citadel, Charleston, SC

Coreids are characterized by the possession of scent glands that secrete both noxious and pheromonal compounds. Some studies suggest a potential role for bacterial endosymbionts in the production of these secretions while other studies suggest the insect can produce the secretions on their own. The metathoracic scent glands of leaf-footed bugs are known to produce a volatile mix of phenolic and terpenoid compounds that have a marked deterrent effect on potential predators and entomologists. While many of these compounds have been characterized, much less appears known about the enzymatic pathways responsible for their production. The leaf-footed bug, *Leptoglossus zonatus*, is a common coreid pest in many agroecosystems throughout the United States. A role for endosymbionts in the production of metathoracic gland secretions in *L. zonatus* has not yet been ascertained. As a first step in addressing this issue, we isolated total RNA from the metathoracic glands of a number of individuals. The RNA was subject to polyA selection and Illumina sequencing. We

obtained 26.5 million clean paired-end reads with 100 bases per read (7.9 Gigabytes total data). We have started the process of *de novo* transcriptome assembly using Trinity bioinformatic software on the Bridges Supercomputer housed at the Pittsburgh Supercomputing Center. Once complete, we will annotate the transcriptome and assess the completeness of biosynthetic pathways and potential contributions by endosymbionts to the production of secretions by the metathoracic glands of *L. zonatus*.

PP206 - Characterization of the lumenal domain of the yeast autophagy protein Atg27

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Autophagy is a catabolic process that is highly conserved in eukaryotes from yeast to humans, brought about by a group of proteins known as the Atg proteins. Autophagy enables cells to recycle nutrients during periods of stress like starvation, and allows them to eliminate damaged cellular components like worn-out mitochondria. Dysregulation of autophagy has been associated with human illnesses such as cancer, lysosomal-storage disorders, and neurodegenerative diseases. Upon induction of autophagy, a temporary double-membraned organelle unique to autophagy is generated anew--the autophagosome. Autophagosomes form while simultaneously sequestering cytoplasmic cargos, ultimately fusing with the degradative organelle of the cell (lysosomes in mammals and vacuoles in yeast), delivering their contents for degradation and providing the cell with a recycled pool of nutrients. One of the Atg proteins, the main focus of our research, Atg27, is a single-pass membrane protein (Cytoplasmic C-terminus and lumenal N-terminus) known to contribute to efficient autophagosome formation. While we know the C-terminus of the protein plays a role in protein targeting to a variety of cellular locations including the Golgi, vacuole, and endosomes, the function of its lumenal domain remains unclear. To test whether or not this lumenal domain is involved in autophagy, we first used site-directed mutagenesis to generate a collection of Atg27 lumenal domain mutants. To detect phenotypic changes associated with these mutations, we used starvation sensitivity, biochemical and fluorescence microscopy assays to quantify autophagic function. Because of the conservation of autophagy in eukaryotes from yeast to humans, an improved understanding of the function(s) of Atg27 and its lumenal domain, will lead to a better understanding of autophagy in human cells and its relationship to disease.

PP207 - Testing Different Blocking Buffers and Concentration effects on signal strength by Western Blotting against Cytochrome C.

Jerod Sharp, Shelby Harris, Roger Sauterer

Jacksonville State University, Jacksonville, AL

Testing Different Blocking Buffers and Concentration effects on signal strength by Western Blotting against Cytochrome C

Western Blotting is a commonly used process in which specific proteins are detected in a sample of tissue or extract by using primary antibodies that specifically bind to the protein and secondary antibodies which bind to the primary antibody. Blocking is the process of exposing a Western blot to a protein or other solution that sticks to the blot matrix and prevents non-specific binding of antibodies. Different blocking buffers give different results depending on the protein being analyzed, with some stripping off the protein while others enhancing the resulting signal. In these experiments, we tested a variety of blocking buffers at different concentrations, as well as combinations of blocking buffers to determine which buffers gave the most substantial signal with little to no background with Western blotting against cytochrome C. Blocking is a very important step during the Western blotting process. As stated previously, it prevents the nonspecific binding of the antibody to the membrane, which is the leading cause of high background in the Western Blot. The high background leads to inaccurate analysis of the proteins within which is what these experiments were aimed to avoid. All experiments used 5% nonfat dry milk as a control. Trial blocking buffers included Milk at concentrations ranging from 1% to 5%, BSA ranging from 1% to 5%, Hemoglobin also ranging from 1% to 5%, Gelatin ranging from 1% to 5% as well, and, lastly, PVP/PEG ranging from 1% to 4% each. Other combinations included PVP/PEG and varying concentrations of different proteins. Since PVP/PEG combinations provided the best signal with Western Blotting against histones, we expect similar results with Western blotting against cytochrome c.

PP208 - The Influence of C5a Receptor on Ovarian Cancer Progression

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Ovarian cancer is the fifth leading cause of death in the United States. It is commonly referred to as the silent killer, because it typically does not show symptoms. Approximately 70% of women are diagnosed in late stages, which causes ovarian cancer to have a low survival rate. Evidence has shown that complement protein C5a can be activated in the tumor microenvironment. Aberrant expression of the C5a receptor (C5aR) has been such detected on such cancers as breast, endothelial, and colon. Several studies have reported that C5a-C5aR axis promotes tumor growth and metastasis. The influence of the C5a-C5aR axis on ovarian cancer progression has not yet been elucidated. We hypothesize that C5aR protein expression will increase with ovarian tumor grade. To test this hypothesis, we performed immunohistochemical staining for C5aR on a tissue microarray slide containing eighty human ovarian cancer cores. Currently, we are imaging random visual fields using light microscopy. Using these images, we will determine a quick score for each patient, based on the amount of C5aR positive cells and the intensity of the stain. Results from this study will allows us to determine if C5aR protein expression is correlated with ovarian cancer grade. Future studies will continue to investigate the mechanisms by which the C5a-C5aR axis promotes ovarian cancer progression.

PP209 - Mammalian Histones and their ability to withstand different Blocking Buffers

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Mammalian histones are highly alkaline proteins found in the nuclei that organize DNA into chromosomes and regulate transcription. We are investigating the interactions between histones and mitochondria by using cell fractionation and Western Blotting to identify the histones. The blocking step in the process coats the membrane with proteins or other molecules to reduce non-specific binding of the antibodies. We use 5% nonfat dry milk as a control for all experiments, it is essential to use this variation of milk because it reduces background noise and helps produce good, clear bands. Although 5% nonfat dry milk is widely used as a blocking buffer, we are testing different blocking buffers to see if the signal strength increases or completely strips proteins off of the blot, the conclusion of which blocking buffer works the best will be determined by the protein being examined. Since antibodies to histone H2A and H2B are low-affinity and give a weak signal, we are therefore testing different blocking buffers, such as milk concentrations ranging from 1 to 5%, BSA ranging from 1 to 5%, and hemoglobin ranging from 1 to 5%, as well as gelatin at 3%, and PVP or PEG individually ranging from 1 to 4% and different combinations of the aforementioned blocking buffers to determine which blocking buffer gives the best detection signal. Our preliminary results indicated that RVR/REG combinations provided the strongest signal, while gelatin tends to strip the proteins completely off of the blot and reduce the signal.

PP210 - Observation of Antipsychotic Medication effects on Mouse Embryonic Fibroblast adhesion and proliferation

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Proper adhesion and morphology are essential to cell survival and proliferation; indeed, disruption of the cytoskeleton disrupts cell survival and proliferation processes. Underscoring its significance, this disruption in the cytoskeleton has been utilized in some cancer treatments as a form of chemotherapy. Antipsychotic medications have disrupting effects on cell morphology and adhesion related to the cytoskeleton that aren't well understood. In this study, a range of concentrations of the antipsychotic chlorpromazine (CPZ) were applied to mouse embryonic fibroblasts and the effects on morphology and adhesion were observed. Typical fibroblast morphology and adhesion to growth surface is lost completely at certain concentrations. At lower concentrations of CPZ, cells have been observed to recover cell morphology and adhesion. Furthermore, the presence or absence of serum in the treatment medium affects recovery, suggesting that growth factor signaling may be involved in this process. Based on these findings, we are now working to understand the mechanism by which fibroblast cells are affected by CPZ. Currently, we are investigating two possible mechanisms, namely that CPZ may be engaging cell signaling cascades via cell-surface receptors or that CPZ may be directly disrupting cytoskeletal filaments. Initially, we are comparing CPZ effects with other known cytoskeletal disruptors. Either of these two possible mechanisms are useful in understanding the effects of CPZ on mammalian cells.

PP212 - The Role of Wisp-1 in Cervical Cancer Cells

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WNT1-inducible-signaling pathway protein 1 (Wisp-1) is a secreted protein that has been shown to promote cell growth and blood vessel formation in several types of cancers. For example, Wisp-1 is found to be over expressed in colon and breast tumors and directly promotes growth factors in cancer cells. The *Wisp-1* gene is upregulated through many mechanisms and promotes malignant transformation through activating the WNT1 signaling pathway. Despite what is known about Wisp-1 and WNT signaling in many cancers, its potential role in one of the most aggressive types of malignancies, cervical cancer, remains largely under explored. The purpose of this project was to identify the role that Wisp-1has in cervical cancer cells. We first assessed the expression of Wisp-1 in a cervical cancer cell line, HeLa. HeLa cell lines were expanded, and we used immuno-fluorescent microscopy to detect the antibodies against Wisp-1. We found that Wisp-1 is significantly increased in cervical cancer cells. These preliminary studies support our plans to assess whether cell proliferation, cell survival, and cell migration/invasion are impacted by the increase of Wisp-1 expression in cervical cancer cells relative to a normal non-cancerous cell line. We hypothesize that Wisp-1, promotes cervical cancer malignancy. Further studies will help us determine whether Wisp-1 is a target candidate for therapeutic intervention or a possible marker for earlier and more efficient detection of cervical cancer.

PP213 - The Effect of Bisphenol-S (BPS) and Bisphenol-F (BPF) on Cancer Cell Metastasis in Zebrafish

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Endocrine disrupting chemicals (EDCs) are natural or synthetic compounds that have the ability within an organism to alter endocrine functions by blocking or mimicking endogenous hormone receptors. Bisphenol-A (BPA) is a chemical used to construct industrial materials, more specifically, polycarbonate plastics and epoxy resins, and it is a well-studied EDC. Exposure to BPA has been shown to lead to an inappropriate activation of the estrogen receptor and development of pre-cancerous mammary lesions. As a result, restrictions have been placed on BPA and other similarly structured compounds have been used in its place, specifically Bisphenol-S (BPS) and Bisphenol-F (BPF). However, it is not known if these structurally similar alternatives are safe. Recent *in-vitro* studies have shown that BPF and BPS can increase cellular proliferation and migration in human breast cancer cells. From these results, we hypothesized that BPS and BPF will increase tumor progression in human breast cancer cells *in-vivo*. To test this hypothesis, zebrafish embryos were microinjected with human breast cancer cells T47D cells and treated with 0.1μM BPS or 1 μM BPF for 4 days. After treatment, zebrafish are analyzed for cell proliferation and metastasis. The embryos are preserved and stained using anti-human KU80 antibody, which detects a protein

found in DNA. The KU80 antibody is specific to human cells and allows for differentially staining of the cancer cells without cross reacting with zebrafish cells. Once the fish have been stained, they are embedded in an agarose-paraffin mixture, sectioned to about 5 µM, and are currently being analyzed by light microscopy for cancer progression.

PP214 - Using environmental DNA to detect the walking catfish (*Clarias batrachus*) in South Florida Waterways

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Invasive species are pervasive in the Florida ecosystem and currently there is an increased number of displaced native species. The walking catfish (*Clarias batrachus*) is an invasive species that has been found in South Florida. Due to it's ability to move from one pond to another, it has spread throughout the freshwater system in South Florida. The voracious nature of the walking catfish has allowed it to outcompete the local Florida fish fauna. Using the ANDe Smith-Root eDNA sampling backpack we filtered water from our local waterways extracted eDNA (environmental DNA) in order to identify types of species present at the sampling site. Our focus is to locate the bodies of water where the invasive walking catfish have spread in order to monitor and control their spread within the Florida ecosystem. We can confirm the presence of species identified by eDNA by electro fishing with the APEX Smith-Root backpack. For comparison, we have extracted the DNA of a walking catfish that we captured and compared it with the eDNA that was filtered out of the water. We used PCR to amplify the mitochondrial gene Cytochrome Oxidase I that is normally used in DNA barcoding. Currently we have only located one live walking catfish in Amelia Earhart Park, but we are continuing to sample local waterways like Snake Creek Park and Miami Lakes and sampling eDNA from filtered water at these sites. In the future we hope to not only use these techniques to find invasive species but to also locate endangered species or to just catalog fish in a certain body of water much more efficiently.

PP215 - Investigating the role of phospho-polyubiquitin in the recruitment and retention of Parkin at the mitochondria using a live cell microscopy approach

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The PINK1:Parkin mitophagy pathway is a quality control process that directs the destruction of damaged, depolarized mitochondria. Mutations within the *PINK1* and *PRKN* genes that encode PTEN-Induced Kinase 1 (PINK1) and Parkin, respectively, are associated with juvenile onset forms of Parkinson's Disease. At polarized mitochondria, the N-terminal mitochondrial targeting sequence of PINK1 facilitates the import of the protein into the mitochondria, where it is cleaved and subsequently degraded by cytosolic proteasomes. On depolarization, PINK1 accumulates at the outer mitochondrial membrane (OMM), recruiting and activating the cytosolic E3 ubiquitin ligase, Parkin, to conjugate polyubiquitin (pUb) on OMM substrates. These pUb chains are phosphorylated by PINK1, creating phospho-polyubiquitin (ppUb), a unique marker of damaged mitochondria that serves as a platform to recruit additional Parkin. The ppUb chains also engage autophagy receptors, facilitating recruitment of the autophagic machinery, leading to the isolation of mitochondria within autophagosomes. However, if mitochondria are repolarized at a sufficiently early stage of this process, PINK1 will rapidly dissociate, aborting the process. We have shown that Parkin dissociates at a slower rate, potentially due to its association with the ppUb chains, which are degraded slowly after repolarization. While disease-associated mutations in *PRKN* have been shown to affect Parkin E3 ligase activity and its recruitment to depolarized mitochondria, it is currently unclear whether these also affect the release of Parkin from the OMM after repolarization. To study the role of ppUb chains in Parkin retention after repolarization, we selected two Parkin mutants with differing E3 ligase activity that are recruited at similar rates to the wild type protein after depolarization and then measured their dissociation rates after repolarization. Specifically, we utilized the hyperactive mutant, W403A, and the E3-ligase deficient mutant, R275W. Our preliminary data indicates that R275W Parkin dissociates more rapidly from the OMM than wildtype Parkin.

PP216 - FGGY Carbohydrate Kinase Domain Containing is Induced During Skeletal Muscle Atrophy and Regulates MAP Kinase Signaling

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Skeletal muscle atrophy can result from a range of physiological conditions, including denervation. To better characterize the molecular genetic events of atrophy, skeletal muscle was isolated from mice following 3 and 14 days of denervation. The gene expression profile of the denervated muscle tissue was analyzed by microarray and compared to control muscle to identify novel atrophy-induced genes. The microarray revealed that FGGY carbohydrate kinase domain containing (Fggy) is expressed in skeletal muscle and is induced in response to denervation. Bioinformatic analysis of the Fggy gene locus revealed two validated alternative isoforms, which we have termed Fggy-001 and Fggy-003, which have distinct transcription initiation sites. In order to confirm that Fggy is expressed in muscle cells, the cDNAs of the two validated alternative variants were cloned from mouse myoblast cells. Interestingly, a novel alternative splice variant for each of the validated alternative isoforms was also cloned from mouse muscle cells, suggesting that at least four Fggy splice variants are expressed in skeletal muscle. Quantitative RT-PCR (RT-qPCR) was performed using RNA isolated from muscle cells and primer pairs that distinguish the four alternative Fggy transcripts. The RT-qPCR data reveals that all four Fggy transcripts are more highly expressed in differentiated myotubes, compared to proliferating myoblasts. Additionally, ectopic expression of Fggy-001 and Fggy-003 resulted in inhibition of muscle cell differentiation and attenuation of the MAP kinase signaling pathway. Finally, confocal fluorescent microscopy analysis revealed that the Fggy-001 transcripts appear to localize to the cytoplasm, while the Fggy-003 transcripts produce a more punctuate localization pattern throughout the cytoplasm of proliferating muscle cells. The characterization of novel genes that are activated during neurogenic atrophy helps improve our understanding of the molecular and cellular events that lead to muscle atrophy and could eventually lead to new therapeutic targets for the treatment of muscle wasting.

PP217 - Effect of Fenbendazole on HeLa Cervical Cancer Cells

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In recent years, fenbendazole and other deworming drugs have gained considerable attention because of their unexpected effects against cancer. Microtubule targeting agents such as Taxol have been approved as anticancer drugs and used widely as they can effectively target fast growing cancer cells by disrupting microtubule dynamics. Antihelminthic drugs also target microtubules. Even though dewormers have greater affinity for helminth tubulin, these drugs can target mammalian tubulins. In this study, we tested the effect of fenbendazole (methyl N-(6-phenylsulfanyl-1H-benzimidazol-2-yl)carbamate) on HeLa cervical cancer cells. HeLa cells were treated with varied concentrations of fenbendazole (0, 100nM, 250nM, 500nM and 1uM) for 24, 48, and 72 hrs. We performed MTT assay to measure the viability of the cells. Metabolically active cells reduce MTT to colored formazan products. This can be dissolved by the addition of dimethyl sulfoxide and quantified by measuring the absorbance at 570nm. We observed that fenbendazole decreases the viability of HeLa cells in a dose-dependent manner. Treating HeLa cells with fenbendazole resulted in apoptosis which was detected by nuclear condensation and chromosome fragmentation using Hoechst staining. Finally, we show that fenbendazole can disrupt microtubule dynamics using anti-tubulin antibody and immunofluorescence.

PP218 - Optimization of a Conditional NF-κB Deficient Microglial Animal Model

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Glioblastoma (GBM) is the most common subtype of adult brain cancer and is extremely aggressive, usually leaving patients only 12 months to live following diagnosis. Part of the aggressive nature of GBM tumors is due to the fact that they are usually resistant to conventional treatment methods such as chemotherapy and radiation. GBM tumors also have a heterogeneous microenvironment, consisting of non-cancerous cells, like microglia, that can promote the tumor. We hypothesize that the NF-κB signaling pathway in microglia positively influences the fast progression and aggressiveness of GBM. In order to better understand microglial NF-κB signaling in GBM progression and whether it influences resistance to treatment, we have created a novel, conditional, animal model that will lack the p65 transcription factor of the NF-κB signaling pathway specifically in microglia upon tamoxifen administration. To make this model a p65fl/fl animal was bred to a Cre recombinase model which is under the control of the microglial specific promoter CX3CR1, as well as tamoxifen regulation. Before GBM studies can begin, tamoxifen dosing for optimal p65 deletion is being conducted, while trying to minimize tamoxifen toxicity. As NF-κB signaling in the central nervous system is naturally low, we are also having to induce an inflammatory response in the animals using lipopolysaccharide so NF-κB levels are high enough to be detected. This may be necessary in order to determine whether tamoxifen administration reduces p65 in non-diseased knockout animals. Precise microglial markers have also been determined for flow cytometry purposes, which will greatly aid in upcoming experiments.

PP219 - Got a Chip on Your Shoulder? Investigating Genetically Modified Corn Chips at Local Restaurants

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Even though the national mandatory bioengineered food disclosure standard (NBFDS) took effect on January 1 of this year and all food packaged and labeled for retail sale must now disclose any bioengineered content in their products, there are still gaps in the new ruling. The NBFDS legislation exempts all restaurants from declaring their bioengineered products, leaving consumers wanting for additional information about what's genetically modified on their dinner plates. While previous studies in the lab investigated major chain restaurants who may have the capacity to provide transparency on the origins of their tortilla chips, this study aims to examine the presence of transgenic crops in the tortilla chips served at independent restaurants throughout the Atlanta area who may not have the ability to trace the origins of their chips. Tortilla chips from three different local establishments will be evaluated for the presence of 2 transgenes frequently found in corn products. *Bt* corn is a common corn product genetically engineered to have its own pesticidal properties, which are derived from *Bacillus thuringiensis*, a soil-dwelling gram-positive bacterium that produces its own innate insecticidal proteins by expressing the Cry genes. DNA will be extracted from samples obtained from each restaurant and the extracted DNA amplified via PCR and analyzed using gel electrophoresis. Established primer pairs will be used to target the novel gene *Zein* in maize and the *Cry1Ab* gene associated with the production of the insecticidal Cry proteins. In order to gather further detect the presence of genetically engineered corn, ELISA will be used to assay the samples for the expression of the Cry1Ab protein. With evidence of genetically engineered corn in the chips from independent restaurants, it may be possible to provide these smaller establishments with information that can assist them to provide the level of transparency that their patrons desire.

PP220 - Does Tulsi and Ashwagandha Have Potential Anticancer Effects?

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Native to India, the herbs Tulsi and Ashwagandha, have been found to have many medicinal properties. *Ocimum sanctum* Linn., also known as Tulsi, or Holy Basil, contains phytochemicals that have anticancer effects by increasing antioxidant activity, altering gene expressions, inducing apoptosis, inhibiting angiogenesis, inhibiting metastasis, and preventing radiation induced DNA damage. *Withania somnifera*, also known as Ashwagandha, Queen of Ayurveda and Indian ginseng, has been found to have anticancer properties by activating p53 tumor suppressor gene. In this project, we studied the effects of Tulsi and Ashwagandha on human prostate cancer cells (PC3) *in vivo*. We used Zebrafish, *Danio rerio*, as our model organism. Our hypothesis is that if we treat PC3 xenotransplanted zebrafish

with Tulsi or Ashwagandha, then we will see a decrease in tumor size. We predict that Tulsi and Ashwagandha will decrease tumor size and decrease tumorigenesis in zebrafish.

We tested the optimal dosage for Ashwagandha and Tulsi on one day old zebrafish embryos. After the optimal dosage was determined, we monitored morphological, physiological, and toxicological effects from the herb treatments. Days one through five, we recorded any differences and similarities of the morphology, the time of hatching, the average heart rates, and the mortality rates of the treated batch compared to the control. On day six, we tested for any cytotoxic effects on the zebrafish through neuronal immunofluorescent labeling. After the optimal dosage was determined, PC3 cells were xenotransplanted into day four old zebrafish. On day five, neuronal immunofluorescent labeling was used to image the tumor. Tulsi and Ashwagandha was then administered to the zebrafish on day five and was monitored daily until day seven. During day seven, neuronal immunofluorescent labeling was used to compare the size of the tumor to see if the cancer cells were still viable. These experiments are still underway.

PP221 - Lichen DNA Barcoding: An Aid in Lichen Identification and Future Air Quality Assessment

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Lichens are model bioindicators of air quality with different classification (crustose, fruticose, and foliose) tolerating varying amounts of pollution. Crustose tolerates the most pollution and fruticose the least. Lichen identification can be challenging in the field. DNA barcoding technology can simplify this process by sampling small amounts of lichens in the field and then extracting the DNA. From there PCR is performed and the results are compared to known samples. The hypothesis is that DNA barcodes of lichens from forest sites will yield more biodiversity and a comparison of sequencing results of similar lichens from different areas will yield a higher mutation frequency in lichens found in urban areas. Lichens in disturbed/undisturbed areas in Nashville, Tennessee were DNA barcoded and the results were compared in BOLD systems, nucleotide BLAST,and to one another. This study is expected to increase knowledge of DNA barcoding as a method of lichen identification and begin to connect genetic differences at the DNA level to varying levels of air quality disturbance.

PP222 - Concentrations of Ethanol and Glutathione on GATA4 Expression and Morphological Deformations in *Ciona intestinalis* Cardiac Development

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Congenital heart defects have been found to be associated with fetal alcohol syndrome in infants due to the consumption of alcohol by pregnant women. Although the development of the cardiovascular system in the human body is extensively complex, *Ciona intestinalis*, a simple tunicate, is a useful model organism to utilize in experimental studies to observe abnormal defects in heart development. GATA4 is a conserved transcription factor that is critical for proper heart development and previous studies have linked alcohol exposure with increased GATA 4 activity. The purpose of this study is to identify the relationship between alcohol and glutathione exposure on the expression of GATA4 in *Ciona intestinalis* heart development. We hypothesized that *Ciona* in the alcohol-treated group will express an increased amount of GATA4 expression and increased defects in heart formation. Glutathione has been shown to mediate the effects of alcohol exposure, so we expected *C.intestinalis* in the alcohol with glutathione treated groups to show normal levels of GATA4 expression and decreased heart formation abnormalities. *Ciona intestinalis* embryos were produced via *in vitro* fertilization and development was observed across 72 hours as the heart formed. Several groups were treated with alcohol and/or glutathione to observe morphological effects of treatment. A control group, with no alcohol or glutathione exposure, was used to compare the results. RNA was extracted from treated samples. RT-PCR and gel electrophoresis were used to measure GATA4 transcription factor expression. Normal development occurred in ethanol administered groups; however, no juvenile formation occurred in glutathione or glutathione plus ethanol treated groups. GATA4 was only detected in adult *Ciona intestinalis* heart samples, but not in embryonic, larval, or juvenile stages. Future work includes additional treatments and quantitative PCR in order to compare GATA4 expression levels.

PP223 - The Role of At5g61470 in Arabidopsis Development

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The seed of *Arabidopsis thaliana* is made of zygotic endosperm and embryo, and an outer layer of maternal seed coat. Immediately after fertilization, endosperm nuclei divide rapidly without cellularization, while absorbing nutrients from maternal tissues. After endosperm cellularization, growth of endosperm slows while embryo growth accelerates as it absorbs nutrients from endosperm. Endosperm is composed of micropylar, chalazal and peripheral endosperm. Being in proximity to the embryo, micropylar endosperm may play a role in regulating the growth and morphogenesis of the embryo. At5G61470, a C2H2 like transcription factor, has been previously identified as a gene expressed in uncellularized micropylar endosperm. Our goal is to understand the role of At5G61470 during endosperm development and how that may affect the interaction between endosperm and the embryo. To confirm expression of At5G61470 in uncellularized micropylar endosperm, its promoter was cloned in front of a GFP reporter gene. The resulting promoter-GFP construct was used to transform Arabidopsis through agrobacterium-mediated floral dip. The analysis of GFP expression pattern in transgenic plants confirmed At5G61470 promoter activity in micropylar endosperm before cellularization. To study the function of At5G61470, a gain-of function approach was used because a loss-of-function mutant (SALK_022934) showed no discernable seed phenotype. The coding region of At5G61470 was cloned downstream of either a double 35S promoter or RGP3 promoter. The resulting constructs will be used to transform Arabidopsis. The double 35S promoter was used to overexpress At5G61470 throughout many plant tissues, while the RGP3 promoter was used to overexpress At5G61470 in cellularized micropylar endosperm. If At5G61470 controls a developmental program specific to uncellularized micropylar endosperm, overexpression of At5G61470 is expected to activate this program ectopically and lead to abnormal phenotype in other tissues, such as leaves and cellularized micropylar endosperm. Over-expression transgenic plants will also allow us to identify

downstream target genes controlled by At5G61470.

PP224 - Somite Patterning and Cellular Fates in Zebrafish Axial Skeleton Development

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Somites are embryonic structures that later give rise to many adult tissues, such as muscle and bone. A sub-compartment of the somite is the sclerotome, which develops into adult tissue of the axial skeletal, such as vertebrae, sternum, ribs, and associated tendons and ligaments. What remains comparatively unstudied is the genetic control of commitment to these fates and when the various tissues are specified. The sclerotome compartment of the somite does not display uniform gene expression, rather there are unique combinations of genes expressed in stereotypical overlapping sub-compartments, and gene expression is dynamic during maturation and migration of the sclerotome. Our work investigates the roles for genes of the *twist* transcription family in directing axial skeletal cell fates from early sclerotome progenitors, specifically tendons and bone precursors. Our studies have found that *twist1b* and *twist2* are important for tendon and Myotendinous Junction (MTJ) formation and these developmental processes are disrupted upon knockdown of these transcription factors. This work will help to define which genes are important in patterning the early sclerotome populations.

PP225 - Generation of Transparent Transgenic Zebrafish Model Organism to Study Microglia Function in Health and Disease Status

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Microglia are the resident macrophages found in zebrafish and humans located along the central nervous system in the brain and spinal cord. These cells act as macrophages, which support the immune system by cleaning any foreign debris. Zebrafish have become versatile models for biomedical research because of their affordable maintenance, transparent body plan during the embryo and larval stages, and genomic accessibility. The purpose of this study is to create an all-encompassing transgenic and transparent organism that has three genetic lines displayed in its genetic sequence. We aim to use zebrafish as an organismal model to study how the microglial cells interact with inflamatiory process including the brain tumor-glioblastoma. To achieve this, we are developing the *in-vivo* transparent transgenic zebrafish modeling system to study the microglia function and manipulation during the adverse condition such as inflammation as well as glioblastoma. Our goal is to study the microglia with reference to inflammation (NF-kB) and cell death (Annexin-5) process. By developing this transgenic phenotype, we have generated the During our study we have grown the individual starins of microglia, Annexin5, NFkB transgenic line as well the Transparent mutant Casper fishes in our facility. As the next step, we paired the breeder from these strain in the following order: 1-Capser-x-Microglia, 2-Casper-x-Annexin5 and 3-Casper-x-NFkB. We cross breeded these breeder and got the F1 generation of trhe mixed population. The larvae obtained from these breeders were screened for the fluroscence expression by using the fluroscent Microcopy. These F1 generation larvae are heterozygous in nature and divided into transgenic and non transgenic group based on the fluroscent exppression. The F1 generation population are raised separately till the adulthood. This Fi generation population are under progress to generate F2 homogyzous progeny to studty the microglia function at health and abnormal condition.

PP226 - Deactivation of FGF9 in Ciona intestinalis with CRISPR/Cas9 gene editing technology

Hannah Lytle, Heather Evans Anderson, Lynn Kee

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The marine invertebrate Ciona intestinalis has a completely sequenced genome, a simple heart with interesting cardiac biology and undergoes rapid development, which collectively provide a useful model organism to study cardiac development. Fibroblast growth factor 9 (FGF9) is a gene that plays a role in cardiac development and is present in both Ciona and vertebrates. The exact role of FGF9 in Ciona is unknown but studies have shown that it is involved in cardiac cell specification. In order to determine the role of FGF9 during development in Ciona, CRISPR/Cas9 was used to edit FGF9 gene sequence in transgenic embryos. We hypothesized that deactivating both exons 1 and 2 of FGF9 will prevent protein formation and result in disrupted heart development in Ciona. Guide RNA sequences were selected and cloned into expression vector. Plasmids the express Cas9 enzyme from a cardiac specific promoter were acquired from AddGene. Ciona embyos were generated via in vitro fertilization and dechorinated to prepare for electroporation of guide RNA and Cas9 plasmids. Fertilization rates were 90+% successful; however, very few embryos developed normally after dechorination. Embryos did not develop at all post-electroporation. Development post dechorination and electroporation is necessary to produce transgenic embryos in order to assess the role of FGF9 in Ciona. Current work is focused on improving embryonic development success post dechorination.

PP227 - Post traumatic regeneration in *Ophioderma brevispinum*.

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Regeneration in brittle stars is well documented, but the mechanisms promoting this process are not. Our study aims to determine which signaling pathways are involved in regeneration and connect that to which cell types are driving post traumatic regrowth. Towards this end we sequenced and assembled the first transcriptome of *Ophioderma brevispina*. This transcriptome was composed of normally re-

generating tissue combined with regenerating tissue, treated with DAPT to pharmacologically downregulate the highly conserved Notch signaling pathway. Notch has previously been implicated in proliferation during neurogenesis, differentiation, cell fate decisions, and other processes. Separate morphological data collected of normal regenerative growth, along with previous other studies, have shown that the radial nerve tissue is driving regeneration. Currently, we are immunostaining neuron and glial cells over time in regenerating nervous tissue which will enable us to understand which cell type drives post traumatic nerve tip growth: neuron or glial cells. This data will then be combined in a project to downregulate Notch with DAPT in regenerating tissue which will be stained to determine which cell type slows or stops proliferating as well as how proliferating cells are migrating. It is known that proliferating radial glia cells replicate during regeneration, but not if Notch is affecting this process alone or in combination with other signaling pathways. All this information will lead to a deeper understanding of regeneration. As a sister group to chordates and vertebrates, echinoderms like brittle stars make an ideal outgroup comparison to help determine why regenerative capabilities were lost to many organisms.

PP228 - Editing FOXO1 gene in Ciona intestinalis using CRISPR/Cas9

Ashley Myers, Heather Evans Anderson, Lynn Kee

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In vertebrates, the FOXO1 gene has been shown to be important during cardiac development and also in the maintenance of healthy adult hearts. FOXO1 is part of a gene family that is highly conserved across chordates. Ciona intestinalis is a marine invertebrate that serves as a useful model organism to study conserved processes across chordates, particularly in cardiac development. Interestingly, adult Ciona are reportedly able to regenerate cardiac tissue across their lifespan. The role of the FOXO1 gene in Ciona intestinalis is unknown. In order to study the role of this gene in Ciona, the gene editing tool CRISPR Cas-9 was used. A guide RNA containing the complementary sequence to the FOXO1 gene was cloned into a plasmid expression vector to be electroporated into Ciona intestinalis embryos created in the lab through in vitro fertilization. Embryos were dechorinated in order to allow for the introduction of plasmid DNA via electroporation to produce transgenic embryos. Developmental success rates post dechorination were recorded after each fertilization and electroporation. Embryos were unable to survive past the electroporation step. For this reason, further research will be conducted in order to determine the cause of embryo death after electroporation.

PP229 - Study on the effect of ectopically expressing InvINH1 by the RGP3 promoter

Tamarah Bratcher

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Appropriate seed development in *Arabidopsis thaliana* involves the coordinated growth between two main components, the embryo and the endosperm. The first stage of endosperm development, known as the syncytial phase, involves the division of the nuclei without forming a cell membrane and cell wall. Following this stage is the cellularization of the endosperm. After cellularization, the growth rate of the endosperm decelerates while embryo growth accelerates. Consequently, the endosperm is eventually absorbed by the embryo. The acceleration of embryo growth suggests that sugar is reallocated from the endosperm to the embryo. Invertase is an enzyme that converts sucrose into fructose and glucose. Invertase has been shown to regulate the movement of sugar from maternal tissues to the endosperm. Our lab identified an invertase inhibitor (*InvINH1)* that is expressed in the endosperm before cellurization. When a ZOU promoter was used to express InvINH1 in the cellularized endosperm, a subtle delay in embryo growth is observed. To strengthen this phenotype, a RGP3 promoter is used to drive the expression of InvINH1. RGP3 promoter is a stronger promoter than that of ZOU. RGP3 interconverts UDP-Arabinopyranose and UDP-Arabinofuranose in the endosperm, which is essential for the formation of plant cell wall. To enhance the delayed embryo growth phenotype, promoter RGP3 was first cloned in front of the *InvINH1* coding region to create vector *pRGP3-InvINH1.* To confirm the expression pattern of RGP3 promoter, the promoter was also cloned in front of a green florescent protein (GFP) reporter. After sequence verification, both constructs were transformed into Arabidopsis plants. After transgenic plants carrying the pRGP3-InvINH1 transgene were identified, a detailed phenotypic analysis was carried out and have preliminary indicated that using the RGP3 promoter to express InvINH1 in the cellularized endosperm could enhance the delayed embryo growth phenotype. Following these preliminary findings, *pRGP3-GFP* will be analyzed also.

PP230 - Survey of Tsuga canadensis (Canadian Hemlock) for the presence of Adelges tsugae (Hemlock Woolly Adelgid) on the Tater Hill Plant Preserve

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Appalachian State University, Boone, NC

Invasive species, such as the Adelges tsugae (Hemlock Woolly Adelgid) have tremendous impacts on native plants. In order to protect populations of Tsuga canadensis (Canadian Hemlocks) randomized population plots will be established on the Tater Hill Plant Preserve to map and record observations on the presence of Adelges tsugae. Surveying stands for the presence of Adelges tsugae will inform the North Carolina Plant Conservation Program if use of biological control is needed for management of the invasive species' population. All trees within the plot will be measured for diameter at breast height (DBH), approximate height, canopy density, GPS coordinates, and severity of Adelges tsugae. This data will establish a base for future research and monitoring of Hemlocks on the preserve.

PP231 - Do amphibian populations at geographic range margins exhibit reduced capacities for phenotypic plasticity?

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Rapid global climate is predicted to eliminate 11 – 17% of species by the end of the century, yet phenotypic plasticity may reduce extinction risk by buffering species from climate change. Such assumptions, however, contradict relationships between genetic diversity and range position, as geographically peripheral populations often exhibit reduced genetic diversity, resulting in populations that may be ill-prepared to withstand climate change. We assessed phenotypic plasticity in tadpoles (Cope's Gray Treefrog, *Hyla chrysoscelis*) from geographically central and peripheral populations in response to two ecological stressors: reduced hydroperiod and predation risk. Tadpoles from peripheral populations exhibited increased growth rates under predation risk and increased tail length: depth ratios, which indicate development towards greater thrust for escape from predators. Data from hydroperiod experiments are still being analyzed, but results to date indicate that peripheral populations may be just as capable, or even more capable, of phenotypically plastic responses to stress. While our findings are limited to small sample sizes from this pilot study, if such patterns are reinforced in more comprehensive future studies, a reconsideration of the hypothesized pattern of central-peripheral variation in phenotypic plasticity, and its roles in response to global climate change, may be necessary.

PP232 - Monarch Caterpillar Survival on a Native and Tropical Milkweed Species

Abigail Culverhouse, Heather Griscom

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This study was initiated to experiment with milkweed species and monarch caterpillars in Virginia. The hypothesis was that *Danaus plexippus* (monarch caterpillar) success and indirectly adult preference would differ between milkweed species. Twelve plants of six milkweed species (5 native to Virginia, 1 tropical) were planted in a garden plot in June 2019. Only two species grew successfully (*Asclepias incarnata* (swamp milkweed) and *Asclepias curassavica* (tropical milkweed)). The total number of caterpillars and 5th instar caterpillars were counted in September and October 2019. Plants were checked bi-weekly for 8 weeks. Once caterpillars reached their 5th instar stage, they were removed and raised to the adult stage in the greenhouse and were released after being tested for the OE parasite. The average height for 12 plants of *A. incarnata* was 750 cm and 14.08 grams with 38 caterpillars, 23 of which were collected as 5th instars. The 12 plants of A. curassavica were slightly taller (778.3cm) and had much greater biomass (37.75 g) but less caterpillars (30 total) and the same number of 5th instars (23). Fifth instar caterpillar count was identical between *A. incarnata* and *A. curassavica*. In the next experiment, 7 species of *Asclepias* will be planted in the garden plot in April 2020. To determine monarch adult preference, eggs will be counted. To determine survival and success, the number of 5th instar caterpillars will be counted throughout the summer months on individual plants. Any adults observed laying eggs will be captured and tested for the OE parasite.

PP233 - Investigating a Salamander Species Community in an Urban Whitehall Nature Preserve

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Salamanders have an important role in upland depression swamps, and for Whitehall Nature Preserve in Charlotte, North Carolina. This study was undertaken in order to determine the presence of *Ambystoma maculatum* (spotted salamanders) and *Ambystoma opacum* (marbled salamander). The spotted salamander was the species of interest since it has not been seen since 2007. Eighteen cover boards were placed throughout a sampling area in the preserve which marks the largest depression swamp. The cover boards were checked four times during November and early December including other cover boards that were previously placed over five years ago. Only marbled salamanders were found under the previously laid cover boards. Since the original project ended sampling of the cover boards occur weekly. The marbled salamanders only being found under the old cover board is not seen as a coincidence. Although it is only speculation the decline of spotted salamanders could be competition, urban development in the area, and whether or not the new cover boards were known or ideal for the salamanders in the short time period.

PP234 - Effects of road salt on growth and development of larval salamanders in the genus *Ambystoma*

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Numerous causes have been implicated in contributing to amphibian population declines, with habitat modification and environmental contaminants being among the most common. This study identifies the effects of a commercial road de-icing salt brand on the growth, development, and mortality of marbled salamander (*Ambystoma opacum*) and spotted salamander (*A. maculatum*) larvae reared to metamorphosis individually, under laboratory conditions. Understanding the effects of increased salinity in aquatic habitats due to surface runoff on the ecology of amphibians is an important part of facilitating the conservation of local amphibian populations. We reared larvae at three salinity levels to evaluate the effect of road salt on salamander fitness. We found significant effects across our salinity treatment levels with respect to mortality, growth, and time to metamorphosis and the patterns of response were similar between the two species. Larvae in both the high (5.0g/L) and medium (2.5g/L) salinity treatments experienced significant mortality compared to the low treatment level (0g/L), but the larvae in the high treatment expired earlier than those in the medium treatment. Larvae experienced a delay in time to metamorphosis in the medium salinity treatment versus the low treatment, but no larvae in the high treatment level reached metamorphosis. The delay in metamorphosis was concomitant with a reduced growth rate among larvae in the high and medium treatments versus the low treatment level. These data indicate that aquatic habitats exposed to environmental contaminants that increase salinity can affect salamander fitness through direct mortality and changes to growth rates and the timing of metamorphosis. The effects we detected in

this study were more severe than similar previous studies reported, indicating the potential for differential responses to salinity across the geographic range of species.

PP235 - The Effects of Hurricane Events on Coastal Strand Gopher Tortoises (Gopherus polyphemus) in St. Augustine, Florida

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Gopher tortoise (*Gopherus polyphemus)* populations in the coastal strand ecosystem of Guana Tolomato Matanzas National Estuarine Research Reserve (GTMNERR) in NE Florida have recently experienced two hurricane events, Matthew (2016) and Irma (2017). We collected data about burrow status and density both pre- and post- hurricane(s) to better understand whether and to what extent this important keystone species is affected by storm-related dune erosion and storm inundation. We tested the hypothesis that the reduction in suitable habitat and forage as well as direct inundation from these hurricanes has reduced this gopher tortoise population.

Data were collected pre-Matthew (Spring, 2016), post-Matthew and pre-Irma (Spring 2017) and again post-Irma (2018) in the coastal foredunes in the northern section of the GTMNERR (approximately 3 linear miles east of A1A). We used researcher observations to classify burrows as either Active, Inactive or Abandoned. We also measured burrow opening width for all Active and Inactive burrows.

We used ArcMap for the geospatial analyses to determine any changes in habitat availability as well as burrow locations. Using ArcMap Desktop and pre-post hurricane imagery, we calculated the area of foredune habitat lost to hurricanes, as well as regrowth of vegetation between hurricanes. We statistically tested for differences in overall burrow activity for each activity category and for changes in burrow size classes.

Sea level rise and the fact that this population's habitat is restricted to the narrow band of dunes between the Atlantic Ocean and State Road A1A raises concerns that this important species is experiencing "coastal squeeze" – coastal habitat loss. It is hoped that our results will help conservation managers understand the threats to this species, determine whether this population is resilient to these threats, and to plan for its conservation.

PP236 - Towards the identification of the soil microbiome community associated with Longleaf Pine

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This project is part of a larger study looking at the restoration of the Long-leaf Pine ecosystem in certain Wildlife Management Areas (WMA) in Northwest Georgia. As part of this larger study another group of researchers has been looking at changes in the plant community in the same plots used for this soil microbiome research. Our long-term aim is to look for potential associations between the above and below-ground community structures.

Although research has shown that the health and composition of the microbiome surrounding the roots of plants has a significant impact on the ability of plants to fight and survive various stressors (Wei et al. 2019), the full extent of the complex system of feedback mechanisms between the rhizosphere and soil microbiome, and the above ground plant communities is not yet understood.

We collected soil samples from six plots located in the Sheffield WMA located in Paulding County, GA. Except for two plots at the savanna site, with slopes south or west facing; soil samples were collected from either north or south facing hillsides. Within each plot, samples were collected in sterile plastic tubes at the center of the plot and 10 m above and below from the center. Five random sub samples were taken from each tube for DNA extraction using a commercially available kit.

Given that plant communities appear to differ between north and south facing slopes, we hypothesize that the soil microbiome will also differ significantly in north versus south facing areas. We also hypothesize that the microbiome in the savanna plots, which are actively being restored for Longleaf pine, will be distinct from all others.

PP237 - Reproductive success of early successional songbirds in intensively managed forests in the Mid-Atlantic Piedmont

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The Mid-Atlantic Piedmont (MAP), a swath of >66,000 km^2 extending from the Virginia-North Carolina border to northern New Jersey, once supported extensive hardwood forests but now is approximately 45% forested with mixed pine and oak-pine types. Key conservation concerns are habitat loss associated with human development and conversion of mixed-species forest acreages to managed plantations. Regenerating forests associated with plantation management provide early successional habitats for a suite of declining bird species such as the Prairie Warbler, a Watch List species that occurs at greater relative abundance here than in any other physiographic region. Though abundance measures provide insights into patterns of patch occupancy, estimates of reproductive success are critical in evaluating quality of habitats and their contributions to population levels. In three field seasons (2004, 2005, 2008) in intensively managed forests in the heart of the MAP, we monitored 178 nests of 10 species and measured vegetation variables at nest sites and habitat patches. Simple nest success was 47% overall and ranged from 53% for Yellow-breasted Chat (24/45) to 13% for Eastern Towhee (2/15). For nests of this "globally significant" Prairie Warbler population, success was 51% (23/45). Using logistic regression to consider variables associated

with nest fate, we found that success did not vary temporally (i.e., year, initiation date) but did vary with microhabitat characteristics (e.g., number of grass stems for Field Sparrow and canopy cover for Prairie Warbler). Preliminary analyses indicate that productivity for some species is less than replacement levels, meaning that some of these managed forests are functioning as reproductive sinks. Though not recently collected, these unpublished data remain very relevant to conservation planning in the MAP and more broadly across Southeastern forests. In our renewed focus on them, we seek to add key reproductive success analyses to complement other studies focused on occurrence and abundance.

PP238 - Variability of CO_2 Flux in a Dry Ephemeral Stream, Riparian Area, and Woodland in an Urban Site in Nashville, Tennessee

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Carbon dioxide (CO□) flux has been widely studied in many environments and locations. One location that is oftentimes overlooked, however, is ephemeral streams. This study looks at the influence of ephemeral streams on the production of CO□. Soil respiration from microbes and roots is expected to be higher in areas that have larger amounts of soil and organic matter than in areas that are rocky or lack organic material. The study was conducted in a deciduous forest at the Belle Forest Cave Property in Nashville, TN during the 2019 autumn by surveying CO□ flux in an ephemeral stream, adjoining riparian area, and surrounding woodland. Each area had five flux collars placed in it and the collars were surveyed a total of ten times over two months using a LI-COR CO□ soil analyzer. The woodland, as expected, had the highest levels of flux while the riparian area and ephemeral stream both had lower levels of CO□ flux. Studies such as this suggest the importance of considering ephemeral streams when calculating CO□ production.

PP239 - Impact of indigenous soil microorganisms on metal uptake of switchgrass (*Panicum virgatum* L.)

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Soil lead (Pb) contamination is a recognized global health problem that has been shown to have adverse effects on both human health. Current methods of remediation of contaminated soil is costly and harmful to the environment. Phytoremediation is a bioremediation process that uses plants as means to remove contaminants from soil in a safer and more cost-efficient way. Arbuscular mycorrhizal fungi (AMF) are microorganisms that form symbiotic relationships with many plants and has been shown to improve a plant's tolerance to metals in contaminated soil. The effect of indigenous species of AMF in soils with varying levels of contamination (soil collected from Decatur, Cedartown, Hickory Grove) on metals (Pb, Al, Fe) uptake by switchgrass (*Panicum virgatum* L.) was studied. Switchgrass was grown initially in 4 different soils, one from each site and a control. Seedlings were then transplanted into 300 mL grow-tubes filled with a 30% moss, 70% vermiculite mixture. Each grow-tube received one switchgrass seedling (15 grow-tubes per treatment). The tubes were kept in the KSU greenhouse and were given a nutrient solution (50 mL) three times per week. After 9 weeks a 3000 ppm Pb solution was introduced (50 mL three times a week) and plants were harvested and processed once lead toxicity was observed.

The foliage of plants grown in soils containing a greater number of AMF species were found to have a statistically significant higher Al concentration between some of the test groups, while the concentration of Pb and Fe in the foliage showed general upwards trends with increasing levels of AMF in the soil. The Fe/Pb ratio in the foliage of plants was higher in plants grown with soil microbes derived from sites of high Pb levels. This suggests that AMF adapt to high Pb content in the soil by increasing Fe uptake of plants.

PP240 - Comparing the Effect of Four Propagation Techniques on Hybrid Chestnut Seedling Quality

Taylor Evans, Heather Griscom

James Madison University, Harrisonburg, VA

Successful restoration of hybrid chestnuts to eastern forests is reliant on both genetic resistance to chestnut blight (*Cryphonectria parasitica*) and the long-term survival and reproduction of resistant individuals. Producing field-ready seedlings able to survive abiotic stresses and compete effectively with existing vegetation will require a renewed focus on seedling quality. Seedling quality is important for successful restoration projects and nursery propagation technique can influence seedling morphology to increase the likelihood of survival. Four propagation methods, bare-root seedlings, seedlings grown in containers, air-pruning raised beds, and the Root Production Method® (RPM®) will be compared across several measures of seedling morphology in order to examine the effects of each method on seedling quality overall. Propagation techniques that utilize air-pruning, such as the raised-bed and RPM®, have been shown to increase the number of first order lateral roots and overall root volume when compared with bare-root seedlings which may lead to greater survival and field-performance. Additionally, RPM® has been shown to produce seedlings with greater basal diameter, height, and a lower age at first fruiting than bare-root seedlings of the same age, though at many times the cost. After one year, seedlings (n ~ 580) will be removed from their growing treatment and measured for height, root collar diameter, number of first-order lateral roots, and root volume to determine the effects of each treatment on overall seedling quality. Seedling quality, planting density, and planting costs are all considered when determining the least-cost approach to achieve a desired stocking density for restoration with seedling quality often compromised. Total cost per seedling will be determined for each treatment by tracking labor hours and overhead costs in order to provide additional information for nurseries growing hybrid chestnut seedlings for restoration plantings.

PP241 - Habitat Suitability Modeling for *Lontra Canadensis* in Southeastern Tennessee

Jordan Allen, Thomas Wilson, Timothy Gaudin

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Predictive niche modeling is an essential tool in effectively managing and conserving wildlife habitats and populations. Through the use of geospatial tools predictive ecological niche models can be developed to better elucidate species habitat suitability and landscape associations. Using environmental and landscape data, we can determine and assign priority areas for conservation efforts targeting *Lontra canadensis* in southeastern Tennessee and beyond. The focus of the present study is the relationship between land cover and use and water quality with otter presence. Using public GIS data collected from Great Smoky Mountains National Park, analysis will be conducted using Maxent to determine habitat suitable for river otters. The results of this study will detail a more comprehensive habitat suitability map for river otters in southeastern Tennessee. This information can be utilized by state officials in managing wildlife and its associated habitats. As river otters are indicators of ecosystem health, maintaining and conserving habitat that is suitable to *L. canadensis* would also mean providing quality habitat for many other wildlife species.

PP242 - Fringed Campion: Conservation and Reintroduction of a Federally Endangered Species

Christian Blasko, Derek Cotton, Mauricio Farinacci, Heather Bowman Cutway

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Silene catesbaei, fringed campion, is a federally endangered perennial herb with rosette forming leaves and pink flowers found along river basins in central Georgia and northwestern Florida. Within this restricted range, fringed campion is mainly threatened by invasive species and habitat loss. In cooperation with the Georgia DNR, we have vegetatively propagated the plant to both augment an established population on private property impacted by invasive species and establish a new population on protected property in middle Georgia. Each population was monitored monthly and observations regarding general plant health, rosette count, leaf count, and survival rates were recorded. The team's principal goal is to successfully establish the fringed campion populations to better understand the environmental factors required for the plant to thrive, including the impact of invasive species removal. A secondary goal is to produce a viable population of fringed campion to further study pollination and propagation without impacting the rare naturally occurring populations.

PP243 - The Effect of Increasing Calcium Levels and Mycorrhizae on American Ginseng

Emilie Fowler, Jacob Peters, Heather Griscom

James Madison University, Harrisonburg, VA

American ginseng (*Panax quinquefolius*) populations have been declining in deciduous forests due to overharvesting and habitat degradation. If ginseng is to be reintroduced, we need to have a better understanding of environmental site conditions, such as soil characteristics, that support robust ginseng populations. We conducted an experimental study with ginseng in the understory of a deciduous forest in the Edith J. Carrier Arboretum in Harrisonburg, Virginia. We tested the effect of adding soil amendments on ginseng growth and survival. We used gypsum to increase soil calcium levels from ~ 3600ppm to ~ 4600ppm and we added inoculant to increase endomycorrhizae spores in the soil. We randomly assigned four treatments from a 2x2 factorial design to twelve subplots and planted ginseng seeds (3 subplots per treatment) in November 2018. In September 2019, we recorded height, leaf area, and percent germination. The addition of gypsum, as well as gypsum and inoculant together, had a significant negative effect on leaf area ($p<0.001$). The addition of gypsum also had a significant negative effect on germination ($p<0.0001$). Height was not affected by treatment. The control treatment had the highest germination rate, with a mean of 38.52% while the two treatments with gypsum had the lowest germination rate of 14.07%. Inoculant had no effect on any measured parameters. Although calcium is necessary for maximizing a plant's nutrient uptake, an excess of calcium cations can also bind to other organic substances, causing a deficiency in soil nutrients. The effect of increasing endomycorrhizae spores in the soil may be more pronounced after several growing seasons. We will continue to monitor ginseng growth and survival for two more growing seasons as the effect of treatment may change with time.

PP244 - Characterizing genetic diversity and population genetic structure in American ginseng, a commercially and culturally valuable medicinal herb

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American ginseng (*Panax quiquefolius* L., Araliaceae) is an herbaceous medicinal plant that is uncommon to rare in eastern deciduous forests of North America. This species is grown worldwide as a commodity crop, but in the Americas it has been wild-collected for centuries, primarily for export to traditional Asian medicine markets. In recent years, ginseng overharvest has led to its designation by CITES (Convention on International Trade in Endangered Species) as a species at risk of extinction. Ginseng may be particularly vulnerable to extirpation events because harvesting often removes larger, older individuals from populations, and plants take at least five years to reproduce sexually. We sampled leaflets from 10-30 individuals per population in eight western North Carolina ginseng populations; harvest pressure and census data varied among populations. We are analyzing microsatellite diversity at seven polymorphic loci in order to understand population genetic structure, estimate genetic diversity, test for gene flow among populations, and relate these factors to harvest pressures. Results can indicate populations' and species' potential for evolutionary response to regulatory protection, harvest, and climate change.

PP245 - Status of the TACF chestnut blight resistance backcross program in Georgia, with emphasis on the Flint seed orchard.

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For more than 35 years, The American Chestnut Foundation (TACF) has focused on backcross breeding as a means of bringing blight resistance into advanced hybrids having a *Castanea dentata* phenotype. A key step has been to develop "backcross orchards" where intercrossed trees of at least 15/16 *C. dentata*; 1/16 *C. mollissima* parentage (BC_3s) were expected to produce at least some offspring as blight resistant as *C. mollissima*. "Seed orchards" planted and culled to contain only highly resistant (BC_3F_2) trees were intended to produce equally resistant (BC_3F_3) offspring for restoration. Recent evidence suggests that highly resistant BC_3F_3s are unlikely to be produced via the original backcross design, due to polygenic inheritance of blight resistance (as opposed to inheritance of a few major effect genes). This has led to a re-evaluation of backcross breeding and questions about how TACF and its state chapter backcross and seed orchards will be used. We focus on the future of seed orchards developed by the Georgia Chapter of TACF (GA-TACF) backcross program. The development of a particular seed orchard, the Flint orchard in Waleska, GA, is detailed as a case study. We propose two key questions that need to be answered going forward: 1) How much blight resistance is necessary for successful restoration? and 2) How phenotypically and genotypically "*C. dentata*" must backcross hybrids be? In addition to calling for more field testing of advanced hybrids, we suggest adding earlier generation trees (e.g., BC_1, BC_2, etc. or alternative crosses such as BC_3 X F_1) to seed orchards and/ or crossing seed orchard trees with transgenic chestnuts (e.g., those containing the OXO gene). We also briefly describe progress and plans for the addition of Phytophthora root rot (PRR) resistance in this breeding program, an important additional need for much of the southern portion of the *C. dentata* range.

PP246 - Identification and Comparison of Arbuscular Mycorrhizal Fungi and Soil Microbiomes Between American Chestnuts and Surrounding Hardwoods

Sarah Andrews, Geoffrey Eger, Paula Jackson

Kennesaw State University, Kennesaw, GA

The American chestnut (*Castanea dentata*) has lived on the brink of extinction ever since chestnut blight was introduced at the start of the 1900s. The goal of this study is to investigate the potential association between arbuscular mycorrhizal fungi and American chestnut plants. Although the symbiotic association between plant roots and arbuscular mycorrhizal fungi (AMF) has been shown to benefit plants primarily through facilitating an increase in nutrient uptake (primarily phosphorous), AMF may also function in the enhanced protection of plants from root fungal pathogens. While there have been studies on the relationship between mycorrhizae and the American chestnut tree; *Castanea dentata*'s diminutive population size and mycorrhizae's mutualistic behavior make it difficult to draw significant correlations between the two, and most of these studies have focused solely on ectomycorrhiza and not AMF.

In this study, we will be researching how AMF species that associate with American chestnut trees differ from their surrounding tree species in north Georgia by sampling in each cardinal direction in a ten-meter radius from individual chestnuts. In addition, through the use of next gen DNA techniques we will examine the microbiome community of chestnut roots and compare them to the surrounding soil and select hardwood plants in the vicinity. In the lab, DNA extraction using a Soil Extraction Kit for both soil and root samples will be performed followed by DNA amplification and replication to identify AMF, plant roots, and soil microbiome communities. All DNA samples will be sent off for analysis. We expect to see similarities in fungal colonization between individual American chestnut trees of different stands and to observe differences between American chestnuts and the surrounding hardwoods. Our hope is that our findings can provide information that will help contribute towards the future mechanisms of revival of American Chestnut populations.

PP247 - Landscape genetics of salamander populations at Mammoth Cave National Park

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Habitat connectivity affects the distribution of genetic diversity among populations by influencing the movements of individuals and the resulting pattern of gene flow across landscapes. Increased isolation between populations decreases genetic variation within populations and increases the risk of local extinction. It has become evident that amphibians are experiencing a period of worldwide population declines brought about by environmental change, and an understanding of the effects of habitat structure on landscape connectivity is important for the development of effective amphibian conservation strategies.The purpose of this study is to investigate the effect of landscape characteristics on gene flow and population structure of the marbled salamander (*Ambystoma opacum*) in Mammoth Cave National Park, Kentucky, USA.Salamander larvae were sampled from 50 ponds and screened at eight microsatellite loci to estimate genetic population structure. We used the R package ResistanceGA to build and evaluate models of landscape resistance using five different habitat categories: coniferous forest, dry deciduous forest, wet deciduous forest, human influence, and surface water. Our results indicate that marbled salamander populations exhibit some genetic structure even over short spatial scales in largely continuous habitat. Our data reveal strong support for an 'isolation by distance' model in which interpond distances are a reliable predictor of the pattern of gene flow observed. However, models of 'isolation by resistance' in which strict interpond geographic distance is modulated by intervening vegetation categories also fit our data well. Overall, the data suggest that marbled salamanders at Mammoth Cave National Park frequently move among breeding ponds, resulting in sufficient gene flow between populations, but that gene flow decreases as interpond distance increases. Furthermore, the movement of individuals is affected by landscape features and heterogeneity of habitats even within this relatively unfragmented landscape.

PP248 - Dendroecology and carbon storage potential of a mature oak-hickory stand in the southern Appalachians

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Disturbance events such as fire and drought play a significant role in forest growth, composition, and structure. Understanding the long term effects of ecological disturbances is increasingly important as climate change continues to exacerbate natural disasters and droughts. Our study seeks to understand the disturbance history and growth rates of a mature oak-hickory stand in Pisgah National Forest, NC. We harvested cross sectional samples from the stumps of 236 recently felled mature trees. Each sample captured the tree's growth rings from pith to bark. By counting and measuring each growth ring, we gain insight into the growth patterns, release events, and ages of each sample tree. The species within the study site were divided into two functional groups based on pore size and water potential; diffuse porous (*Acer* and *Liriodendron*) and ring porous (*Quercus* and *Carya*). We hypothesize that the diffuse porous species will be more sensitive to past disturbance events compared to ring porous species. In addition, we are interested in understanding the carbon storage potential for the site. Private landowners as well as industrial timber organizations have a growing interest in a forest's ability to sequester and store carbon. However, the effect climate change will have on carbon storage remains unclear. The objectives of this study are to 1) establish a growth and disturbance history of the stand via dendrochronology and tree ring analysis and 2) quantify the carbon storage potential for each species. We hope to better understand how past disturbances, especially drought, have impacted growth and carbon storage of species prominent throughout the southern Appalachians.

PP249 - Historical vegetation reconstruction at two Piedmont remnant grassland sites suggests dominant role of Native American burning

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Historical accounts suggest the presence of expansive upland grasslands in the eastern Piedmont, these hypothesized to have hosted the numerous endemic and Midwestern-affinity heliophytes now primarily relegated to areas of frequent disturbance. As, in the absence of disturbance, the vegetation climax in the region is forest, some have suggested that putative grasslands were largely maintained by fire return intervals significantly shorter than at present. However, the frequency of fire and whether fire was primarily natural or human-caused remain controversial issues. No matter the cause of fire, if indeed occurring at the estimated rates over the past hundreds of years, temporally stable grasslands and savannas would indeed likely have resulted. Interestingly, the carbon isotopic signature of such systems should be readily discernible from d13C analyses of soil organic matter (SOM), which thus represent an indirect test of long-term frequent fire. To address this issue, we focused on two putative grassland remnants in the North Carolina Piedmont, well-known for their Midwest prairie-affinity flora. We sought to analyze d13C of SOM at both sites to test the hypothesis that the historical vegetation class of both sites was grassland up until European settlement, at which point the class transitioned to forest. We found: (1) no evidence of C4-dominated grasslands at any point in the past 2000 years, (2) a general trend toward more closed canopy conditions that began prior to European arrival, and (3) pronounced temporal fluctuations in degree of openness of vegetation between woodland, savanna, and forest. As the fluctuations appear not to be associated with reconstructed regional climatic patterns, we hypothesize that they reflect shifting human activity over time, suggesting that periods of open vegetation over the past 2000 years resulted from a rate of burning by Native Americans that was significantly higher than the natural fire frequency in the area.

PP250 - Inadvertent Damage to Non-Target Trees Due to Timber Removal and Equipment Transport

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Damage to trees by logging equipment along the travel route (within the park) to the timber-harvesting site was observed at San Felasco Hammock State Preserve Park. This was a 200-acre salvage harvest operation in response to the presence of southern pine beetles (*Dendroctonus frontalis*) in loblolly pine (*Pinus taeda*) within the park boundaries in the summer of 2018. One of the purposes of the harvest was to remove trees that are infected with southern pine beetles, with the goal of preventing them from moving into the upland pine community dominated by long-leaf pine (*Pinus palustris*) trees within the park. Along the logging vehicle travel route (1.9 miles), sixty trees were damaged, 37 were hardwoods and the remainder pine. The damage were assigned values of 1-4, one being the least amount of damage, rubbing of bark, four was the highest level of damage, broken limbs and or deep cuts into tree. Some trees had multiple injuries but at different levels. Level 2 was assigned to trees that had bark removed and the phloem or cambium were visibly exposed. Overall, the majority of injuries (two-thirds) was classified at a level two. Of the *Pinus* species that were injured on this route, 22.7 % were infected with black turpentine beetles (*Dendroctonus terebrans*). This species of beetle is often found in stressed or injured trees but it is not likely to kill the tree. This amount of damage in such a short travel distance has significant management implications. In 2019, the trees on this route area were removed for a long-term restoration plan.

PP251 - Urban Development Intensity and Impervious Substrate Cover as Minor Factors in Measuring Urban Plant Diversity

Faith Martin, Darlene Panvini

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Urban plant communities are an integral component of urban sustainability. However, urbanization increases levels of impervious substrates such as roads, sidewalks, and buildings, thus posing a considerable threat to the long-term viability of urban plant communities. With higher intensity of development, plant diversity was expected to decline and change in community composition. Using 10 m^2 quad-

rats, plant diversity was surveyed in a Nashville neighborhood with varying levels of impervious substrates and development intensity. Quadrats with higher development intensity exhibited higher plant diversity. Increased plant diversity may be explained by historical, socioeconomic, and ecological factors that result in decreased plant competition, more variety in plant installations, and changes in habitat. Defining urban environments based on development intensity undermines the complexity of land use in urban ecosystems. Understanding the complexity of urban environments and plant communities can equip cities to mitigate the consequences of climate change facing urban environments, as urban plant communities can provide cities with crucial ecosystem services such as stormwater management, cooling, and overall enhancement of biodiversity.

PP252 - Remediation of Heavy Metals from Wastewater

Caleb Guerra, Caleigh Eberhardt, Bal Khatiwada

Abraham Baldwin Agricultural College, Tifton, GA

Clean water is crucial for healthy life. As the population of the world is growing every day, there are more factories and industries being established to fulfill the demand. Industries such as mining, painting, pest control, textiles dyes, tannery, and electroplating produce heavy metal as waste. The waste is often washed through running water, which eventually reaches to our water system. In our lab, we are planning to collect water samples from different sites and test for concentration heavy metals using inductively coupled plasma-optical emission spectrometer (ICP-OES). We plan to test for filtration material that is effective for removing those heavy metals. We will test filtration ability of conventional activated carbon and compare the results with filtration ability of diatomaceous earth (DE). DE is of special interest to us because of its porous nature and has polar functional group on the surface called silanol. We will modify DE with graphene oxide (GO) to use it for removal of heavy metals and compare the results with bare DE. We will test the adsorption ability of DE and DE-GO to heavy metals using Langmuir Adsorption Isotherm.

PP253 - Evaluating mammal diversity across habitats fragmented by a power line cut

Behil Alemu, Christopher Brown

Georgia Gwinnett College, Lawrenceville, GA

The constant transformation and expansion of cites due to population growth and urbanization negatively impacts the habitat of native mammal species. Habitat loss and habitat fragmentation can affect population size, movement, species richness, and genetic diversity. Georgia Gwinnett College is located in Gwinnett County, one of the fastest growing regions of the Atlanta metro area. This study was conducted to evaluate the diversity and movement of mid-sized to large mammals living in a wooded area on the Georgia Gwinnett College campus but which is split by a human-made corridor created by a power line cut. Diversity was measured using motion-detecting trail cameras. Time spent in an area was approximated by the number of pictures taken of each species. Cameras were placed in three different locations: (1) in a small patch of woods closer to campus and which contains a moderately used trail, (2) in the power line cut, and (3) in a larger wooded area distal to campus and the power line cut and further from human disturbance. Our results indicate there is more diversity of mid- to large-sized mammals in the wooded areas on either side of the power line cut compared to within the power line cut. Mammals also spent more time in the larger wooded area away from human disturbance than in the wooded area closer to campus and much less in the power line cut.

PP254 - An Ornamental Plant Found Spreading Aggressively: Potential Invasiveness of *Dryopteris erythrosora* (Dryopteridaceae) in North America

Hannah Umstead, Tom Diggs

University of North Georgia, Oakwood, GA

Dryopteris erythrosora (D.C. Eaton) Kunze (Dryopteridaceae) is an exotic fern native to Asia; it is often sold in nurseries in the United States and used in landscaping. In the summer of 2017 while collecting plants for BIOL 3329K (Identification of Vascular Flora) at the University of North Georgia, the authors noticed a dense population of *D. erythrosora* in a disturbed suburban woodlot, located in Alpharetta, Georgia. A population survey at the site documented many fertile fronds and the recruitment of young plants. The results were published in December of 2018 in *The American Fern Journal*, citing other recent works which documented similar occurrences. Additional populations in Georgia have since been discovered and are noted here, along with an update on the original population in Alpharetta. Although *D. erythrosora* has not been considered invasive, the data collected suggests that it is capable of reproducing and maturing into well-established colonies in the wild.

PP255 - Tree growth and survival in a one-year CREP restoration project in the Shenandoah Valley, Virginia.

Heather Griscom

James Madison University, Harrisonburg, VA

Riparian buffers protected from livestock are an extremely important ecological tool that land managers can use to protect local streams and waterways to improve water quality, biodiversity and prevent soil erosion. In this study, twelve acres along a stream within an active pasture were fenced-off and replanted through funding from the Conservation Reserve Enhancement Program (CREP). In the spring of 2019, 539 saplings representing 17 different species were planted, placed within a 4" tree shelter, tagged, mapped and measured for initial height and diameter. After one growing season (fall 2019), diameter and height were remeasured in addition to mortality and evidence of deer browse. Sugar Maple (*Acer saccaharum*), Bald Cypress (*Taxodium distichum),* Silky Dogwood (*Cornus amomum)*, and Black Cherry (*Prunus serotina)* had significantly greater survival (100%) compared to Sycamore (*Platanus occidentalis*) which had the lowest

survival rate (73%) ($p < 0.05$). Height and diameter growth rate was also significantly different between species ($p < 0.05$). Black Locust (*Robinia pseudoacacia)* had the greatest height growth rate (81.2 cm/year) while River Birch (*Betula nigra)* had the lowest height growth rate (-6.38 cm/year). Sycamore (*Platanus occidentalis*) had the largest diameter growth rate (6.6 cm/year) while River Birch (*Betula nigra)* had the smallest diameter growth rate (-.48 cm/year). The goal of this long-term study is to determine which tree species have the greatest growth and survival in the presence of deer herbivory (above the tree shelters) and on limestone soil. Planted trees will continue to be monitored for the next five years.

PP256 - Host specificity patterns of commensal invertebrates in Tampa Bay

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Sponges are a major constituent of marine environments, providing stable habitat for a variety of commensal invertebrates. Ascidians are also host to marine invertebrates, but the ephemeral nature of ascidians provides a less stable habitat. Natural seasonal fluctuations in commensal invertebrate abundance are expected, especially in the ephemeral ascidian hosts. *Styela plicata* (Lesueur, 1823) is a relatively common non-native ascidian that is an important biological host on hard-bottom environments in Tampa Bay. *Haliclona* (*Reniera*) *tubifera* (George & Wilson, 1919), *Cliona celata* Grant, 1826, and *Spheciospongia vesparium* (Lamarck, 1815) are common sponge species often found occupying the same hard-bottom habitat in Tampa Bay. Competition for hosts among generalist commensal organisms may exist, especially in the winter months when there are fewer ascidians available. Seasonal collections of ascidians and sponges were completed in Tampa Bay and commensal associates were identified to the lowest taxonomic level possible. Preliminary results include host preference patterns for some organisms while other organisms inhabit any of the collected hosts. A positive correlation between sponge host size and abundance of associates is expected and a shift in abundance of commensal organisms from ascidian to sponge hosts in winter is predicted. Further analysis of data will highlight the importance of each host and the potential impact of a non-native species on the Tampa Bay community.

PP257 - Molecular Exploration of the Cnidarian Genus *Aequorea*in Europe: Are Morphological Species Supported by Molecular Data?

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Members of the genus *Aequorea* (crystal jellies), are pelagic hydrozoans found throughout the global oceans and occasionally recorded from Norwegian waters in the NE Atlantic. Species within the genus are difficult to identify using morphology only, due to plastic characters, and it has been argued which species occur in Norwegian waters. A total of 27 *Aequorea* species are known worldwide, including 4 nomen dubium, and most species are known from Pacific Ocean as well as NW Atlantic. However, the definitive number of species is uncertain because the genus is poorly studied. We gathered *Aequorea* records from Norwegian waters, through citizen science and online search, from 2009 to 2018. We also sampled, identified and analyzed *Aequorea* specimens from Haganes/Sotra near Bergen City, Norway and the Mediterranean Coast of Turkey. Morphological features were all concordant with *A. forskale*a Péron & Lesueur, 1810. We plan to sequence cytochrome oxidase 1 (COI) and internal transcribed spacer 1 (ITS1) to identify specimens and construct a phylogenetic tree to assess species relationships in our samples. Our results will help to begin to clarify the species relationship in this understudied genus. Our results may suggest the presence of cryptic species, or may suggest combining some of the currently described species. This would advance our understanding of the systematics of this group of jellyfish beyond our current limited understanding.

PP258 - Titanium Dioxide (TiO_2) Nanoparticles in a Freshwater System: Trophic Transfer and Ecotoxicity in a Simple Aquatic Food Web

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Titanium dioxide (TiO_2) nanoparticles (NPs) are commonly used in many industrial applications; they are present in a large range of products including paint, textiles, paper, cosmetics, food packaging, plastics, and sunscreen. Nanoparticles released into the environment are largely expected to end up in aquatic ecosystems—thus, their fate to aquatic organisms is of great concern. Many research studies to date have focused on the toxicological effects of TiO_2 nanoparticles to aquatic organisms. Less attention, however, has been given to understanding how TiO_2 NPs affect intricate ecological processes such as the trophic interactions in aquatic food webs. The aim of this study was two-fold: (1) to establish the acute toxic effects of TiO_2 nanoparticles on surface and deep-residing algal species and (2) to determine if the potential for trophic transfer of TiO_2 nanoparticles differed between surface and deep-residing algal species to algae-eating shrimp. Spirogyra and Oedogonium were chosen to represent surface and deep-residing algal species respectively. The results of this study show that Spirogyra and Oedogonium exhibited cell wall disruption in the presence of TiO_2 and latex bead nanoparticles. The nanoparticle treated algae were consumed in each treatment by algae-eating shrimp. Algal material was easily visualized through the transparent body of the shrimp. In conclusion, TiO_2 and latex-bead NPs showed significant damaging effects on green algae and possible trophic transfer of these materials in aquatic food webs.

PP259 - Understanding Biodiversity Through Taxonomic Training

Sally Sir, Kristine N. White

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Amphipods are important bioindicators that can be found in almost any body of water. The presence of amphipods can provide an abundance of information about the environment. However, amphipods are frequently misidentified, rendering most of the information gained from them unusable. This issue has highlighted a need for taxonomic training. The goals of this project include teaching students various methods used in amphipod taxonomy, including collection, dissection, identification of amphipods. Equally important is that students understand the role of amphipods in their environments. In addition to traditional morphological taxonomy techniques such as scientific illustration, students will learn to use a stacking imaging system to create more detailed photographs useful in identification. Proficiency in these types of skills benefits the fields of taxonomy, ecology, and conservation while providing a set of skills that students can use throughout their careers. Once trained, students will apply their skills to a National Science Foundation funded project focusing on Caribbean amphipods of Panama. The project will ultimately result in a revisionary systematics monograph describing the regional amphipod diversity and identification tools for both experts and non-experts. The methods listed here will be described and potential applications of the project results by non-experts will be presented.

PP260 - Chasing cane toads: locomotive and behavioral changes from northward dispersal

Steven Gardner, Arthur Appel, Mary Mendonça

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The cane toad (*Rhinella marina*) is an invasive species in southern Florida, and expanding populations are predicted to have higher locomotive capacity. To assess endurance of toads from Florida, toads from a northern (New Port Richey (NPR)) (n = 24) and southern (Miami (n = 20)) population were placed into a 1.83 m long track and tapped to encourage movement. A principal component analysis was performed on the number of taps, hops, and time it took for the toads to stop moving. The first component, "unwillingness to move", (fewer taps and hops, and shorter time until movement stopped) characterized 91.65% of the data variation. NPR toads traveled less far than Miami toads ($p = 0.01$), and NPR cane toads were more unwilling to move compared to Miami cane toads ($p = 0.005$). Another toad subset (n = 38 (Miami) and n = 34 (NPR)) was placed inside of a mechanical locomotion setup, where they were forced to move until reaching exhaustion. Each toad was immediately removed, bled to obtain lactate levels, and then allowed to rest. Toads that traveled further had higher lactate ($p = 0.05$). When forced to move, NPR toads traveled 5.12 ($\pm$ 1.78) m further than Miami toads ($p < 0.01$), and NPR individuals had lower lactate at exhaustion than those from Miami ($p = 0.03$). Lactate levels decreased with increasing toad mass ($p = 0.01$), and decreased more in Miami compared NPR cane toads ($p = 0.04$). Lactate decreased over time in resting toads ($p < 0.01$), although the rate of which was the same for both populations ($p = 0.78$). These results indicate behavioral and endurance changes have occurred in these toads from northward dispersal.

PP261 - Herbarium and Field Studies of Metal-Hyperaccumulating Plants from Ultramafic Soils in Guatemala

Haley Disinger, Joe Pollard

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Recent discovery of metal-hyperaccumulator plants in the Neotropics prompted further exploration of the ultramafic areas of this region. The most extensive serpentine and nickel-laterite deposits in Central America occur in eastern Guatemala. Recent developments in X-ray fluorescence analysis technology allow rapid, nondestructive measurement of specimens in the field and in herbaria. A survey of herbarium specimens from the Izabal Department of Guatemala, targeting genera known to hyperaccumulate metals elsewhere, revealed several new hyperaccumulators, as well as their general distribution of hyperaccumulation. Recent studies in Mexico have discovered nickel hyperaccumulation in *Orthion* spp. (Violaceae). In Guatemala, *O. subsessile* was found to hyperaccumulate nickel and occasionally cobalt, and *O. montanum* is newly reported to hyperaccumulate nickel, with concentrations exceeding 5000 µg/g. *Chionanthus panamensis* (Oleaceae) is a new facultative hyperaccumulator with an extensive geographic range stretching from southern Mexico to Panama and displaying nickel concentrations approaching 5000 µg/g. *Arachnothryx linguiformis* (Rubiaceae) is a new obligate nickel hyperaccumulator, and the first species in its genus (previously included in *Rondeletia*) known to hyperaccumulate any metal. This species is endemic to areas around Lake Izabal, Guatemala, and seems to live exclusively on ultramafic substrates. Subsequent plant collection and corresponding soil sampling at several sites in Guatemala revealed relatively consistent foliar nickel concentrations across populations, with no significant correlation between soil and plant nickel concentrations. The maximum nickel concentration observed in *A. linguiformis* was >1% of dry weight, with a mean ~3800 µg/g. None of the newly discovered species are promising candidates for phytoremediation or agromining, but they present interesting cases for conservation and research.

PP262 - The effects of monoterpenes on the growth of mistletoe radicles (*Phoradendron leucarpum*)

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Sam Houston State University, Huntsville, TX

Mistletoe (*Phoradendron leucarpum*) is a common aerial parasite throughout the Southeast United States. Within that range mistletoe host preference varies without any known cause. Locally, mistletoes seem to prefer one or two potential host species, even when other potential host species are present. We hypothesize that this preference is influenced by the pattern of host monoterpene emission in late winter when seeds have germinated, because monoterpenes have been shown to positively influence the growth of seedling radicles. However, the mode of emissions of host plants has not yet been ascertained; monoterpene release may take place in a burst early in the season, or it may occur steadily throughout the growing season. Further, some potential hosts (like pecan) produce high quantities of

monoterpenes constitutively. To investigate the effects of monoterpenes on radicle growth, we introduce plated mistletoe seeds to one of three monoterpenes (pinene, limonene, myrcene), as well as a control (10% DCM). Monoterpenes were administered in quantities typical of herbaceous plants in steady state over 10 weeks, in a "burst" of 10X that concentration delivered once, or in 10X concentration delivered over the course of the semester. Seed growth towards monoterpene or control was quantified digitally. In the absence of the ability to measure monoterpene emissions accurately from host plants *in situ*, this may demonstrate correlation between growth and patterns of monoterpene production a controlled setting.

PP263 - Exploring patterns of thermal acclimation of leaf respiration in a marsh-mangrove ecotone

Matt Sturchio

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This project focuses on better understanding aboveground C fluxes of Spartina and mangroves in relation to temperature (over space and time and with warming). We plan to test whether C fluxes from leaves acclimate to seasonal temperature changes across sites that differ in seasonality, whether C flux responses to temperature across seasons and sites differs for Spartina (*Spartina alterniflora*)and black mangrove (*Avicenna germinans*), and whether warming inside chambers alters how species respond to temporal and spatial changes in temperature. At the global scale, respiration is the second largest flux of C (behind photosynthesis), and ~50% of respiration comes from leaves. But there remains little info on respiratory C fluxes in marsh/mangroves over space and time. Respiration is also a key parameter for global models that predict climate-carbon cycle interactions which are related to sea level rise; coastal systems are poorly represented in these models. By developing this data we are providing new information that has both local and global implications.

PP264 - Community Level Physiological Profiling of the Microbiome on Organic Farms versus Conventional Farms in the Bluegrass Region, Kentucky

Ryleigh Bonk

Midway University, Midway, KY

Soil includes bacteria and fungi that make up the soil's microbiome. Organic farms enhance biodiversity by supporting the microbiome in the soil with natural means of care. Conventional farms support their soil with chemical fertilizers, pesticides, herbicides, and other harmful systems. The purpose of this study was to compare the Community Level Physiological Profiles (CLPP) of organic farms versus conventional farms. Soil samples were collected from four farms, two organic and two conventional, in the Bluegrass region of Kentucky from August 2019 to October 2019. To determine the CLPP of each farm, soil samples were diluted, put into wells of an EcoPlate, and then ran through a plate reader for five days. Three out of the four farms had an optical density (OD) greater than 0.25, which indicates community richness. Although these farms had community richness, the between-farm difference was not significant enough to conclude that the CLPP was different between organic and conventional farms. There was also no significance between the soil during and after the drought. One farm in particular, proved to be an outlier with much lower OD values. The results failed to reject the null hypothesis and indicated that there was no significant difference in the microbiome of the soil between organic farms and conventional farms.

PP265 - Impact of changing climates on an Ornamental *Rhododendron* species

Hannah Houston, Megan Buzard, Liliana Rangel-Parra, Howard Neufeld

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Plant ecophysiology can be used to help researchers understand the mechanisms that enable plants to respond to future climate change. Global change is causing many ecosystems to experience warming and altered precipitation regimes, which could impact the functionality of many plant species. Rhododendrons (Ericaceae) are common shrubs in the southern Appalachians, and include both native species and horticultural varieties. They are evergreen and may retain leaves for 3-7 years, depending on habitat and species. We measured gas exchange and water relations on variously aged leaves of ornamental (*Rhododendron. sp.*) and native (*R. maximum*) shrubs during the winter months. Both ornamental and native species exhibit leaf nyctinasty and rolling when leaves are frozen, which previous studies suggest reduces photoinhibition. However, there is little information about the capacity for leaves to carry out gas exchange during warm days in winter. We measured the ecophysiology of these shrubs during fall and winter 2019-2020. During this project the southern Appalachians experienced an unprecedented drought and three ornamental rhododendrons were intensively monitored to determine their response. Using a Scholander Pressure Chamber, we measured predawn and midday leaf water potentials at peak drought (Nov 14) when potentials reached remarkably low values (-4.7 $\pm$ 0.2 and -14.4 $\pm$ 0.3 MPa, respectively), indicating severe water stress. Gas exchange was measured using a Li-6800. On a cold day (~20 ^{o}C), photosynthesis reached 1.0 µmol m^{-2} s^{-1}) while stomatal conductance was low (< 0.1 mol m^{-2} s^{-1}), indicating nearly closed stomata. On a warmer day (12 ^{o}C), maximum rates reached 5.8 µmol m^{-2} s^{-1} and 0.07 mol m^{-2} s^{-1}). On some sunny days, leaves could be 13 ^{o}C warmer than air temperatures. These results suggest carbon uptake can occur in winter. If climate change increases the frequency of warm winter days, annual carbon budgets may be altered for these shrubs.

PP266 - Eye Size is Related to the Proportion of Frogs in the Diets of North American Watersnakes (genus *Nerodia*)

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The evolution of a trait depends on its function as well as its phylogenetic history. In snakes of the family Colubridae, the evolution of eye size and consequent visual acuity has been related to habitat use. One clade of colubrid snakes, the watersnake genus *Nerodia*, utilizes aquatic habitats where they feed primarily on fish and frogs. Because capturing frogs may require greater visual acuity than catching fish, we tested the hypothesis that eye size and placement in watersnakes is related to the proportion of frogs in the diet. We measured

eye diameter and head size, the latter as a surrogate variable for snake size. Then we determined eye placement from angles using the computer program FIJI (just ImageJ) from images taken from rostral (dorsal versus lateral placement of eyes) and dorsal (lateral versus anterior placement) views. We calculated pairwise genetic distances from 1082 bp of the cytochrome b portion of the mtDNA genome. We then tested for phylogenetic signal in the statistical program R v. 3.6.1. Detecting no signal, we used standard statistical analyses to test for a potential relationship between (1) eye size, (2) eye growth, and (3) eye placement and the proportion of frogs in the diets of watersnake species. We found significant relationships between eye size and frog proportion and between eye growth and frog proportion but not for eye placement. *Nerodia fasciata* and *N. erythrogaster* have the largest eyes of the genus. Moreover, unlike those of their congeners, the eyes of these two species enlarge allometrically with growth. Adults of both species heavily on frogs, shifting from a piscivorous diet as they grow. Our results support the hypothesis that eye size and presumably visual acuity in these two species is related to their ability to capture frogs.

PP267 - To tree or not to tree: arboreality shapes signal size across but not within species of a diverse lizard genus

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Animals have adapted and diversified to fill the numerous habitats on earth. It is well understood that microhabitat use can shape many aspects of an animal's ecology, such as food availability, proximity to predators, and access to mates. However, comparatively less is known about how habitat preference may influence other aspects important to an animal, such as communication. Male lizards in the genus *Sceloporus*, are found in a variety of habitats across the United States and Mexico, and have a complex signaling system involving displays of colorful belly patches. Microhabitat use varies across and within species (ex. arboreal and terrestrial lizards), as does patch size. Thus, this study system presents an excellent opportunity to examine macro- and microevolutionary patterns of signal evolution. Here, we take a two-pronged approach to understand how habitat shapes colorful signaling patches. First, we implement modern phylogenetic comparative methods to examine evolutionary consequences of microhabitat use on signal size across 54 *Sceloporus* lizard species. Next, we conduct a detailed empirical study within a single species to understand how habitat shapes communicative signals on a much finer scale. We find that across species, arboreality constrains signal size. Arboreal species have much larger signaling patches, and it is very evolutionarily difficult for them to lose their color signals. However, within a species, there is no impact of microhabitat use on signal size. This study highlights the strength of a comparative approach for revealing broad patterns of signal evolution that cannot be detected within a single species.

PP268 - Geometric morphometric analysis of candidate species within Desmognathus fuscus

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Recent work in our lab has uncovered multiple candidate species within the widely-distributed complex of the Northern Dusky salamander, *Desmognathus fuscus*. Evidence for genetic divergence includes both mitochondrial and nuclear sequence data. However, little is currently known about morphological differences among these newly-found lineages of *D. fuscus.* We conducted geometric morphometric analyses to check for variation. We assembled photographs of *D. fuscus* specimens, representing eight different mitochondrial clades, in tps file format and plotted twelve homologous landmarks on each image using the program tpsDig. We then produced a series of dorsal and ventral measurements using Morpheus software. In order to control for size, we converted the raw measurements into ratios, which we statistically analyzed in R software through independent sample t-tests comparing different lineages. Our analysis suggests that there are statistically significant examples of morphological deviation between some of these clades.

PP269 - Landscape genetics of a Fundulus spp. hybrid zone in Northeastern Florida

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Hybridization, the interbreeding of diagnostically distinct populations, is relatively common in both animal and plant taxa whenever reproductive isolation is not complete. Studies of hybridization are essential for understanding processes related to speciation, the regulation of species ranges, and the role of ecology in each of these processes. Two closely related killifish species (F. heteroclitus and F. grandis), overlap in range and form a narrow hybrid zone along part of Northeastern Florida. Little is currently known about the extent of hybridization between these two species and whether their respective ranges are associated with any environmental parameter. Therefore, a study was conducted to assess the spatial genetic patterns of the hybrid zone in an attempt to determine: 1) the current edges of the hybrid zone, 2) whether the hybrid zone is environmentally determined or not, and 3) if any environmental patterns correlate with the genetic patterns. Samples of fishes were collected from 10 locations spanning the putative range of the hybrid zone (~40 km) at regular intervals. Each fish was genotyped at four highly differentiated loci (3 nuclear and 1 mitochondrial). Patterns of genetic differentiation among sites were determined utilizing STRUCTURE and environmental parameters of predominant vegetation (mangrove and salt marsh grasses), temperature and salinity were tested for correlations with observed genetic patterns. Strong evidence for a mosaic hybrid zone was found suggesting an environmental component to the spatial patterns of the hybrid zone, however, none of the environmental parameters tested correlated strongly with the genetic patterns.

PP270 - Parentage and mate choice in the invasive Joro Spider (*Nephila clavata*) in Georgia

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An invasive species can be any organism that is inhabiting an ecosystem where they are not native and in which they cause harm. Invasive species can cause harm to both flora and fauna especially when their populations are large. Joro spiders (*Trichonephila clavata*), belonging to the genus of golden silk orb-weavers, are a new inhabitant of North Georgia. Native to Asia, the female Joro spider is known for its 3-D web, large size, and brightly colored abdomen. This makes the species easy to spot and identify, along with their high abundance. The females can reach up to 5 centimeters in length while the males tend to be about a third of the size. The females wrap 1 sac containing about 400-1500 eggs in a protective silk coating which then overwinter. While the adults die off around the onset of winter, eggs hatch in spring and develop into juveniles which mature into adults in fall. Multiple males are commonly spotted in a female's web at a time. This raises the question of whether the males compete to mate with the female or if the female mates with multiple males, essentially hedging her genetic bets. There has been no observations of the female's preference in courting behavior in the invaded range in Georgia. We are interested in answering the question of whether there are more than one male spider contributing sperm to one egg casing. Using three microsatellite markers from a closely related spider, we plan to perform parentage analysis to assess the number of males fathering offspring with a particular female. Our research could suggest that only a single male is allowed to mate with a particular female, or that multiple mating occurs in Joro spiders.

PP271 - Genetic diversity of an isolated population of the Ocoee salamander (*Desmognathus ocoee*)

Alaina Choiniere, Emily Bewick, Carlos D. Camp, Jessica A. Wooten

Piedmont College, Demorest, GA

Biodiversity loss is occurring at a rapid rate due to anthropogenic changes to the natural environment. One aspect of biodiversity loss is the loss of genetic diversity. A community of lungless salamanders inhabiting a stream on the campus of Piedmont College in northeastern Georgia was isolated by stream diversion during past construction. Previous work on the mitochondrial gene *COX1* (~600 bp) in the Ocoee salamander (*Desmognathus ocoee*) and the black-bellied salamander (*D. quadramaculatus*) from the same site showed no significant genetic structure between Piedmont College and Hazel Creek. On the other hand, evidence from the nuclear gene *POMC* for two species of brook salamander (genus *Eurycea*) indicated reduced genetic diversity at this site. Therefore, we measured the possible impact of human disturbance on genetic diversity of this isolated population of *D. ocoee*. We collected samples from two undisturbed populations, Nancytown Creek and Hazel Creek in northeastern Georgia, in addition to the population at Piedmont College. We analyzed genetic diversity and gene flow utilizing the nuclear gene *POMC* (~550 bp) and compared our results to previous findings at this site.

PP272 - Chromosome evolution in Spiraea

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Spiraea virginiana Britton (*Rosaceae*) is a federally-listed rare, clonal shrub that inhabits riparian zones within the Ohio River drainage. The species often occurs in areas of high disturbance and predominantly uses asexual reproduction to propagate from populations upstream. Although the species' known range suggests that sexual reproduction played an important role in its evolutionary history, sexual reproduction is currently almost non-existent. Pollination studies have shown that the species can produce fertile seeds; however, this has not been witnessed in wild populations. Understanding the role of chromosome evolution within the genus may provide some insight towards understanding the sexual reproductive barriers experienced in this species. A consensus phylogeny was generated by combining several published phylogenies and chromosome number was mapped to identify patterns of chromosome evolution. The base chromosome number for the genus is n=9 and multiple independent polyploid events have occurred within the clade. Polyploidy events could be driving the reproduction patterns of the genus Spiraea. It is important to map chromosome number by species to try and identify relationships based on phylogenetic distance.

PP273 - Identifying Candidate Species within the Northern Dusky Salamander Species Complex

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Recent work in our lab has uncovered multiple candidate species within the widely-distributed complex of the Northern Dusky salamander, *Desmognathus fuscus*. Evidence for genetic divergence includes both mitochondrial and nuclear sequence data. We collected genomic data from numerous populations representing each of the newly found lineages of *D. fuscus*, and analyzed it in R software, using a variety of statistical methods. We used DAPC to identify and describe clusters of SNP data within and between lineages and populations. We used the function snapclust for maximum-likelihood genetic clustering and were able to infer relationships between clusters by using the conStruct method.

PP274 - Exploring connectivity among Gulf Coast tick (*Amblyomma maculatum*) populations through comparative population genetics

Sara Simmons[1], RIP Bio Class 2018-2019[1], Holly Gaff[1,2], David Gauthier[1]

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The Gulf Coast tick, *Amblyomma maculatum*, is the primary natural vector of the bacterium *Rickettsia parkeri.* Recently established *A. maculatum* populations in Virginia tend to have high prevalence of *R. parkeri*, a pathogen that can be passed transovarially from the female tick to her offspring. The factors contributing to high *R. parkeri* prevalence in Virginia are not known, but investigating connectivity between colonized sites can help determine whether sites with higher prevalence are either isolated or well-connected to each other through migration, thus serving as a source of infected individuals. We characterized 16S rRNA haplotypes of *A. maculatum* and the closely-related *A. americanum* collected from sites where these species co-occur. This comparison allows us to identify distinct patterns in the Gulf Coast tick that could be explained by differences in host preferences or landscape barriers compared to *A. americanum*. We explored connectivity and genetic structure among Virginia populations using pairwise φ_{ST} and AMOVA analyses. Our study identified one recently restored native grassland site with low *A. maculatum* haplotype diversity and strong evidence of a founder effect, whereas most sites are haplotypically diverse, but significantly different from each other in terms of haplotype frequency, with no clear genetic structure or connectivity between sites. These findings contrast with a slight mainland/island structure between *A. americanum* populations. Our results suggest that *A. maculatum* populations occasionally arise following long-distance drop-offs of few individual ticks in suitable habitat, but no clear migration corridors were observed. The distinct population genetic patterns between species can be explained by differences in host preference particularly if the Chesapeake Bay interrupts migration of *A. americanum* but not *A. maculatum*. Going forward, we will increase the genetic resolution to characterize individual ticks using genome-sampling techniques such as ddRAD, and expand the geographic area studied to include additional populations.

PP275 - Circularized Mitochondrial mRNA Fragments in a Human HEK Cell Line

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The relatively recent focus on the widespread occurrence and abundance of circular RNAs (circRNA) in the human cell nucleus has sparked an intensive interest in their existence and possible roles in cell gene expression and physiology. The presence of circRNAs in mammalian mitochondria, however, has been under-explored. Mitochondrial mRNAs differ from those produced from nuclear genes because they lack introns and are transcribed as poly-cistronic transcripts that are endonucleolytically cleaved, leaving transcripts with very small 5' and 3' UTRs. Circular RNAs have been identified in the semi-autonomous organelles of single-celled organisms and plants but their purpose has not been clearly demonstrated. The goal of our project was to test the hypothesis, processed mRNAs are circularized in vertebrate mitochondria as a necessary RNA processing step prior to translation. Mitochondrial mRNAs were isolated from the human cell line HEK293 and evidence of circularization sought by treating RNA with RNAse-R and then amplifying putative 3'-5' junction sites. Sequence results demonstrated the occurrence of mRNA circularization within each coding region of the mitochondrial genome. However, in most cases the circRNAs carried coding regions that had been truncated, suggesting they were not translatable. Quantification of the circularized versions of the mRNAs revealed they comprise a small portion (~10%) of the total mRNA. These findings demonstrate that mRNA circularization occurs in mammalian mitochondria but it does not appear to play a role in making translatable mRNAs.

PP276 - Determining the Significance of SLC6A1 Variant 468 C R in Myoclonic-Atonic Epilepsy and Autism via Bioinformatic Analysis

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SLC6A1 is a gene that encodes for a GABA transporter responsible for the reuptake of GABA from the space around the synapse after neural stimulation has occurred. The rare genetic disorder SLC6A1 epileptic encephalopathy is caused by a dominant, non-inherited mutation in SLC6A1, resulting in the loss of the transporter protein function. This condition is noted by the development of seizures within the first few years along with mental retardation and behavioral issues disorders found on the autism spectrum. An analysis performed by the biotech company HudsonAlpha discovered many variations in the gene of those affected with this disorder such as the variant 468 C R which has been found in association with myoclonic-atonic epilepsy but the significance of this is currently unknown. Along with this discovery, data collected on this variant by Michigan State University, a comparison of the amino acid swap in #468 from Cysteine to Arginine (C to R) in a known patient exhibiting clinical symptoms was performed. Compiled metrics and statistics comparing this variant to all the known variants listed in ClinVar, TopMed and GnomAD as well as evolutionary comparison to 225 species has established a method for determining the impact of this variant as it relates to other known samples. It also has a high possible impact for motif involvement in the development of the disease. This indicates that a variation in amino acid sequence in this location is highly likely to result in deleterious effects on the patient. This protein will be modeled using YASARA software to observe the change that has happened to the protein. Using graphs and databases, I've shown that 468 C R is very similar to the patient variant giving more cause to the idea that this variant mostly likely causes the disorder.

PP277 - Genetic analysis of *Staphylococcus aureus* biofilm production pathways blocked by novel lead compounds.

Luke Jones, Payal Patel, Sutton Scarboro, Linda Hensel, David Goode

Mercer University, Macon, GA

Bacteria utilize a complex chemical communication system—a process known as quorum sensing. This mode of intercellular communication affords bacteria the ability to assess densities of chemical signaling molecules, also known as autoinducers. In turn, autoinducers target specific chemical receptors, and through signal transduction cascades, promote changes in gene expression. One such response is the formation of an extracellular biofilm. Fifteen novel compounds were previously found to possess anti-biofilm properties in *S. aureus*. Our current approach utilizes the successes of such compounds to analyze the genetic pathways involved in *S. aureus* biofilm formation. Additionally, we emphasize the importance of testing various drug structures in order that we may investigate the possibility for multiple points of inhibition through the multitude of biochemical pathways responsible for biofilm production. Using EMS mutagenesis, twelve *S. aureus* mutants were isolated for diminished biofilm production. We have since analyzed phenylalanine-trans-3,5-difluorocinnamic acid, tyrosine-trans-3,5-difluorocinnamic acid, tyrosine trans-3-chloro-2-fluorocinnamic acid and tyrosine trans-2-chlorocinnamic acid for anti-biofilm properties in four of the mutagenized strains. After duplication, our results show promise in identifying potential biofilm-producing biochemical pathways inhibited by novel compounds. Additionally, future work will include drug variants such as: glycine trans-3,5-dibromo-4-methoxylcinnamic acid, tryptophan trans-3,5-dibromo-4-methoxylcinnamic acid and tyrosine trans-3,5-dibromo-4-methoxylcinnamic acid, all of which significantly inhibit wild type *S. aureus* biofilm formation.

PP278 - SLC6A1 I220V is Projected to Not Impact Protein Function but Could Cause Epilepsy

Britney Barker[1], Benjie G. Blair[1], Jeremy Prokop[2], Richard Watkins[1]

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SLC6A1 is a gene in humans that codes for one of the main GABA transporter proteins in the central nervous system. This protein is associated with an autosomal dominant disorder that can cause epileptic encephalopathy. A variant at the 220 amino acid position is classified as a missense mutation that causes myoclonic-atonic epilepsy and is a result of Isoleucine being improperly replaced with Valine. This variant has not yet been clinically reported in individuals experiencing physical symptoms linked with an SLC6A1 related disease. Statistical comparison of this gene in humans to 225 other species containing the same gene was performed and aligned, where each codon was then studied for long term stability. The variant is presented with an unknown significance and a low impact score of 6 on a scale of 0 to 148.5 with a relative correspondence to other known benign variants of this gene. According to Align-GVGD, I220V is a Class 0 missense and is suspected to be least likely to affect molecular function. However, since this variant has been identified to cause myoclonic-atonic epilepsy, a model of the gene with this variant was conducted to determine molecular shifts in the transmembrane bound proteins that may have unexpected impacts when used as a transport protein for key ligands.

PP279 - Determining Cause and Heredity of the Expression of Duchenne Muscular Dystrophy in a Female Carrier

Emily Payne, Jessica Nicks

Anderson University, Anderson, SC

This study examined the genetic basis and heredity of a proband that is a symptomatic female carrier of Duchenne Muscular Dystrophy with a deletion involving exon 45. The proband's family includes an unaffected father and older brother, while the mother and identical twin sister have the deletion but remain fully asymptomatic. As a recessive X-linked disease, the rarity of a symptomatic female for DMD cannot be understated. This study explored the method of inheritance in this family through various techniques. Creatine-Kinase levels were first examined in the proband and the twin sister to confirm that only one was truly symptomatic. X-inactivation testing led to a need to perform PCR of a large section of the X chromosome throughout the family to examine the possibility of recombination in the mother through further analysis of the amplified DNA. After determining the true mode of inheritance, RNA isolation from fibroblast cell lines, reverse transcriptase, and RT-PCR were performed to analyze expression levels in an attempt to discover the cause for the varied phenotypes between the twin daughters. Sequencing of this product led to further insight into the root cause of this varied expression of symptoms among the female carriers. With the findings of homologous recombination, highly skewed x-inactivation, and expression levels, this study gained further insight into a rare case with great implications for other x-linked illnesses and a further understanding of Duchenne Muscular Dystrophy.

PP280 - Characterization of Differential Expression Patterns throughout Development of the Trembler-J Mouse Model for Charcot-Marie-Tooth Syndrome

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Mutation and abnormal expression of the peripheral myelin protein 22 (PMP22) is causative of one the most common inherited peripheral neuropathies in humans, Charcot-Marie-Tooth 1A (CMT1A) disease. The heterozygous Trembler-J (*Tr^{J}/+*) mouse is a model for PMP22-associated peripheral neuropathy characteristic of CMT1A. Although its function is not completely understood, *PMP22* is differentially expressed in neural and non-neural tissues, where it is thought to be involved in proper myelination of peripheral nerves and control of normal cell growth and differentiation, respectively. As a means of understanding the role of *Pmp22* in non-neural tissues, temporal patterns of gene expression were evaluated in non-neural tissues throughout embryonic and post-natal development of the Trembler-J mouse. In this study we used mRNA Differential Display to profile the Tr^{J}/+ transcriptome in non-neural tissues throughout embryonic (E9.5-E17.5) and postnatal (D1-D42) development. At each developmental time point, differentially expressed sequences were cloned and sequenced to identify genes of potential importance to normal tissue development. Using the technique of mRNA Differential Display,

we have identified 85 differentially expressed genes, 25 of which were validated by quantitative reverse transcription PCR (qRTPCR). Ontological classification revealed dysregulation of genes primarily involved in cell communication and signal transduction (21%), regulation of nucleic acid metabolism (20%), protein metabolism (14%) and cell growth and/or maintenance (13%). Sequence analysis of the upstream region suggests that transcription factors in the EGR family may be common regulators of this set of genes. Our analysis shows that several genes are differentially expressed relative to the copy number of non-mutated *pmp22* alleles. We predict that the collective interaction of these genes may be important to cellular processes central to the development of tissues, in which *pmp22* may be functioning as a *Gas* gene.

PP281 - Ichthyofaunal evidence supporting a hypothesized stream capture event between the Tennessee and Mobile River Basins and implications on conservation

Julia Wood[1], M. Worth Pugh[2], Phillip Harris[2], Thomas Near[3], Richard Harrington[3], Michael Sandel[1]

[1]University of West Alabama, Livingston, AL, [2]The University of Alabama, Tuscaloosa, AL, [3]Yale University, New Haven, CT

Alabama and Tennessee exhibit the greatest freshwater biodiversity in the United States. The Tennessee River and Mobile River basins are physically divided, but historical and recent natural history collections reveal evidence for inter-basin transfer of aquatic fauna. We report recent collections of three cold-water fish species (*Etheostoma nigripinne, Chrosomus tennesseensis,* and *Rhinichthys obtusus*) from headwaters of the Locust Fork of the Black Warrior River, Alabama. The headwaters of the Black Warrior River and tributaries to the Tennessee River are in close proximity and our results suggest that these species may have colonized the upper Locust Fork either through avulsion of surface streams or flow diversion within the subterranean aquifer. We conducted preliminary genetic analyses using two mitochondrial genes (COI and *cytb*). Results suggest there are differences between the populations in the headwaters of the Locust Fork and the respective previously established distributions of each fish. Furthermore, we discuss the implications of these collections on the mechanisms that drive biodiversity, including how stream capture may have isolated these populations leading to potential speciation events. We outline further areas of investigation and conservation efforts.

PP282 - A preliminary assessment of chloroplast sequences in *Coccoloba uvifera* (Polygonaceae) for use in phylogeographic analyses

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The Citadel, Charleston, SC

Coccoloba uvifera (sea grape) is a tropical member of the Polygonaceae family and a significant component of coastal habitats along the Atlantic, Caribbean, and Pacific coasts of the neotropics. This native tree species occur at the beach – forest transition where it provides important habitat and food for animals, stabilizes habitat during tropical storms, and has been shown to improve sea turtle nesting success relative to nesting on exposed beaches. We collected *C. uvifera* leaves from mainland (Belize, Panama, Mexico) and island (Aruba, Curacao, Antigua, Trinidad, Tobago, Bahamas, Puerto Rica, Jamaica, and the Dominican Republic) locations across the neotropics. As a preliminary analysis, we used two mainland (Belize, Panama) and two island (Aruba, Antigua) samples to survey six non-coding chloroplast regions. Four intergenic regions and an ndhA intron yielded high-quality sequence results. These five plastid sequences were concatenated for each of 19 individuals, yielding sequences approximately 4675 bases in length with 21 variable and potentially informative sites. Eleven insertions/deletions (INDELS) were coded by the simple gap coding method. Network analysis identified 14 haplotypes from the 19 individuals. Genetic relationships among haplotypes were complex although plants from Belize were clearly different from Aruba, Antigua, and Panama samples. Haplotype diversity decreased from Aruba (5) to Panama and Antigua (4) to Belize (3). The level of variation observed in the five informative chloroplast regions analyzed thus far suggests continued sequencing of these regions in additional samples should provide sufficient variation to facilitate phylogeographic analyses of *C. uvifera* radiation in the Caribbean region.

PP283 - Longitudinal metabarcodes analysis of the aquatic prokaryotic microbiome of a karst Appalachian cave in Natural Tunnel state park, VA, USA

Kendall Morse, Robert VanGundy, Bruce Cahoon

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Caves are often assumed to be static environments separated from weather changes experienced on the surface. For example, the temperature of a cave remains near 10-12 degrees Celsius all year with near 100% humidity. The stability of these subterranean environments makes them attractive to many different animals (e.g. troglodytes, eutroglophiles, and subtroglophiles) as well as microorganisms such as bacteria and protists. The water found in caves originates from either underground or the surface. This water may be filtered by overlying soils or contaminated by human activities on the surface, such as- agriculture, garbage, and sewage disposal any of which can alter cave environments. The purpose of this study was to use metabarcoding to monitor the aquatic prokaryotic microbiome of a cave for one year and compare it to nearby surface water. Water samples were collected in triplicate from two locations inside of Panel Cave in Natural Tunnel State Park in Duffield, VA and two locations outside of the cave. Of the two cave locations, one was fed by groundwater and the other by surface water. These samples were filtered, DNA extracted, the 16S V4 region PCR amplified, and sequenced using MiSeq technology. 991 unique prokaryotic ASVs were detected from cave samples and 131 (7.9%) were not found in surface samples. PCO analysis demonstrated a clear delineation between cave and surface microbiome. Most surprisingly, there was a cave microbe population and diversity boom in the Fall months, while on the surface, counts and biodiversity remained relatively steady all year.

PP284 - Genetic structure of black bass in northern Georgia lakes

Taylor Bates, Michael Erwin, Elizabeth Harrison

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Species identification aids in fishery management's efforts to maintain biodiversity within water systems. Spotted bass (*Micropterus punctulatus)* and Alabama bass (*Micropertus henshalli)* have similar morphological characteristics despite no close genetic relatedness, and the Georgia Wildlife Resources Division classifies both species as "spotted" bass. In the southeast United States, spotted bass populations are distributed across the Tennessee River basin, while native Alabama bass populations are found in the Coosa River Basin. Both are known to have been introduced to the Chattahoochee River Basin, and Alabama bass are suspected to have been introduced into lakes in the Tennesee River drainage. Populations classified as "spotted" bass have expanded in the Chattahoochee and Savannah River drainage, to the detriment of other black bass populations, namely the Smallmouth bass. This project employs the use of microsatellite markers and the universal barcoding mitochondrial gene COI to achieve species identification within and among populations containing black bass with similar morphological characteristics. From three sampling sites in north Georgia, Lake Blue Ridge, Lake Chatuge, and Lake Nottely, fin clippings from 288 fish were obtained for mitochondrial DNA analysis and forty-eight black bass samples from each lake were used to investigate population genetic structure employing 15 microsatellite loci. These analyses indicate that all three lakes contained genetically similar populations, with no detection of spotted bass individuals in the population sampled.

PP285 - Analyzing Genetic Structure of Brown Trout (*Salmo trutta)* and Rainbow Trout (*Oncorhynchus mykiss)* Populations Inhabiting Waters Below Buford Dam on the Chattahoochee River, Georgia

Mitchell Shivers, Michael Erwin

Georgia Gwinnett College, Lawrenceville, GA

Historically, the brown trout and rainbow trout populations below Buford Dam have been supplemented by stocking. The frequency of stocking is dependent on a stream's fishing pressure, accessibility, and water conditions (GDNR). Stocking of brown trout was terminated in 2006, as brown trout were naturally reproducing at high rates and sustaining viable populations below the dam (GADNR-WRD, 2012). Population supplementation may influence genetic population structure, thus the need for molecular monitoring. Brown trout and rainbow trout have been collected at three different sample sites along 15.76 miles downstream of Buford Dam on the Chattahoochee River. Genetic structuring of both species will be analyzed utilizing mitochondrial cytochrome oxidase subunit 1 (CO1) gene and ribosomal protein gene for intron 1 (S7) to reveal haplotype and nucleotide diversity.

PP286 - Possible Phytochemical Correlation with Genetic Distance in *Solidago altissima*

Nicholas Walker, Ray Williams, Matt C. Estep

Appalachian State University, Boone, NC

Solidago altissima is a widespread old-field plant species that exhibits considerable intraspecific genetic variation. This species is considered a foundation plant species in many disturbed habitats and supports a large insect community. Previous studies have found that genotypes vary in dominant insect herbivore abundance, and that part of this response is due to differences in leaf phytochemistry among genotypes. What is unknown is the role of the genetic structures (measured as genetic distance) contribution to chemical variation, and thus possibly insect abundance. To investigate this, leaf samples of *S. altissima* were taken for genetic analysis and quantification of volatile terpenes, previously identified by the Williams lab group as a key phytochemical group in this system. Naturally occurring patches (i.e. genotypes) from eight sites covering a portion of this plants geographic range from western Illinois through Iowa were sampled. To determine possible effects due to genetic distance, genotypes within sites (close proximity) and across sites (distant proximity) were compared. DNA was extracted using CTAB then amplified via PCR with microsatellite markers. Genotype data will be compiled to create a distance matrix for analysis. Potential correlations between terpene concentration and genetic distance measures will use a Mantel test. For numerous volatile terpenes identified, we found significant effects both within and across sites, though not each compound varied at each level. For some compounds there was a tendency for sites closer in proximity to have similar concentrations of terpenes, though this was not evident in every case. Should genetic distance correlate with terpene variation at the genotype and/or site level, this analysis will contribute to a greater understanding of how genetic variation in *S. altissima* affects phytochemistry as found in previous investigations.

PP287 - Using non-invasive sampling and citizen science to assess microsatellite polymorphism in the Appalachian eastern spotted skunk (*Spilogale putorius putorius)*

Kiersten Keith-Pedersen, Jake Shields, Brian Wuertz, Liesl Erb, Alisa Hove

Warren Wilson College, Asheville, NC

The eastern spotted skunk *(Spilogale putorius)* is a threatened mesocarnivore once common in the eastern and central United States. Since the 1940's, *S. putorius* populations have experienced major declines and may have reached numbers as low as 1% of their historical sizes. Our project's long-term aim is to evaluate the genetic diversity of *S. putorius* in western North Carolina through the analysis of microsatellite markers. Past genetic studies of eastern spotted skunks have focused on the plains subspecies (*S. p. interrupta*), with limited assessment of microsatellite polymorphism in the Appalachian subspecies (*S. p. putorius*). A critical first step in understanding the population genetics of this subspecies is determining which genetic markers show polymorphism in this part of the species' range. To begin this process, 35 hair samples were obtained via hair snares from a single North Carolina population in Spring 2017. We are currently optimizing protocols for DNA extraction from hair samples. Following extraction, PCR protocols will be optimized for amplification of 5-8 microsatellite loci, with subsequent confirmation of PCR success through agarose gel electrophoresis. Samples will be analyzed using microsatellite fragment analysis to determine individual genotypes. We are also establishing a regional monitoring program involving

game cameras, hair snares, and citizen scientists, which will generate additional samples beginning in Spring 2019. At the meeting we will present an overview and discussion of microsatellite variation in the population studied here, which can indicate the Appalachian spotted skunk's potential for evolutionary responses to regulatory protection and environmental change. Also included will be a summary of any modifications to hair snare deployment procedures and its implementation by citizen scientists.

PP288 - Determining the Genetic Similarity and Relatedness of *Rosa* Varieties using RAPD Analysis

Allison Wright, Medhini Urs, Brittany Gasper

Florida Southern College, Lakeland, FL

The lineage of the genus *Rosa* can be traced mostly to Asia with some species originating in North America, Europe, and Northern Africa. Rosarians have crossed and hybridized roses all over the world from their original form, called antiques, into their multiply-double modern variants. This has created new species and hybrids. Though some rose lineages were thoroughbred, open-air pollination has led to the discovery of unintended and commercially viable species. Often with open-air fertilization the mother is known, while the pollinator is not. As a result, many rose species and varieties have unknown origins. Various antique roses are so similar they could be considered the same species but are referred to by different names by their respective breeders. This study looked to understand the relatedness between eleven different rose varieties. Seven of these rose varieties are believed to be hybrids of the true China rose and may be single mutation variants of each other or may be more distantly related. Two of these rose varieties may be identical to each other, and the other two rose species represent either a mother-offspring relationship or a self-pollinating seedling relationship. The relatedness of these rose varieties was determined using RAPD DNA analysis with five different RAPD primers. A summary of the rose relationships from the RAPD analysis and what this means moving forward with rosarian classifications will be discussed.

PP289 - The Role of *FIS2* and *AGL62* in regulating the expression of *InvINH1* and *InvINH2* in *Arabidopsis thaliana*

Ruqiyah Mukarram, Dongfang Wang

Spelman College, Atlanta, GA

Angiosperm seeds are embryonic plants enclosed in seed coats. During double fertilization, the egg cell and the central cell are fertilized by two sperm cells, which give rise to the embryo and the endosperm, respectively. In plants with nuclear endosperm, such as Arabidopsis, the endosperm enters a syncytial phase after fertilization, when the endosperm nuclei undergo mitosis without cytokinesis. After endosperm cellularization, the endosperm experiences cell death and is eventually absorbed by the embryo. Our lab had discovered that two invertase inhibitors (InvINH1 and InvINH2) produced in the embryo-surrounding region of the endosperm are capable of suppressing embryo growth during the syncytial phase. In this study, we investigated whether InvINHs expression are regulated by two known regulators of syncytial endosperm development, FIS2 and AGL62. InvINH1 and InvINH2 promoter-GFP fusions were first introduced into *fis2* or *agl62* mutant background. GFP expression was then analyzed in mutant plants that were homozygous for the promoter-GFP transgene. Our data indicated that both InvINH1 and InvINH2 promoter-GFP fusions were up-regulated in *fis2* mutant, and down-regulated in *agl62* mutant, suggesting that FIS2 and AGL62 are the repressor and the activator of InvINHs expression, respectively. Since FIS2 is known to suppress AGL62 expression, we have identified a linear pathway that activates InvINHs expression after fertilization and represses InvINHs expression after endosperm cellularization. This precise timing of InvINHs expression in the syncytial endosperm is likely required for the proper coordination of embryo and endosperm growth during early stage of seed development.

PP290 - Investigating suppressors in the karrikin pathway of *Arabidopsis thaliana*

Lauren Cheek, Jack Xhemali, John Stanga

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Karrikins (KAR) are a family of molecules found naturally in burning plant material that regulate plant growth by signaling through the F-box protein MORE AXILLARY GROWTH 2 (MAX2). The loss of function mutant, *max2,* results in longer hypocotyls, inhibited seed germination, smaller cotyledons, increased shoot branching, rounded leaves, and more. SUPPRESSOR OF MAX2 1 (SMAX1) and SMAX1-LIKE 2 (SMXL2) function as negative regulators in response to KAR. The purpose of this study is to determine downstream components of the karrikin pathway by identifying possible suppressors of *smax1 smxl2* mutant phenotypes. In a previous mutant screen, possible suppressors were determined by hypocotyl length. To further characterize these mutants, hypocotyl length and cotyledon area were recorded from red light grown seedlings and adult plants were measured for rosette shape, height, branching, and other phenotypes.

PP291 - A Survey of Viral-Infected Roses in the Collection at Florida Southern College

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Plant viruses can cause many diseases in all types of crops and ornamental plants. Some viruses cause noticeable flaws to infected plants, ranging from mild discoloration to major deformities and, in extreme situations, death of the plant. However virus infection can also be symptom-free where infected plants display no outwardly obvious signs and appear otherwise healthy. Undetected infections can have serious consequences for all plants, particularly agricultural crops that are transported worldwide and ornamental plants that are important parts of gardens and collections. Prunus necrotic ringspot virus (PNRV) and Apple Mosaic Virus (AMV) are two RNA viruses that cause infections in several species of plants, including the *Rosa* genus that contains all species of roses. PNRV causes ring spot diseases and can be easily spread through plant propagation methods, pollen, and infected seeds. In addition to ring spots, PNRV-infected plants can show reduced leaf size, though these symptoms do not usually show up until one year infection, after which the symptoms for many plants will disappear. AMV can be transmitted through root grafting, propagation equipment, or sap, and while some plants will show leaf

symptoms, many plants will appear asymptomatic. This study aimed to survey the rose collection at Florida Southern College (FSC) for plants infected with PNRV or AMV. The FSC Rose collection contains two gardens that house approximately 375 roses between them. The college has one of only two rose mosaic virus heat therapy programs in the United States and is a source of mosaic-free propagating material to nurseries around the US and internationally. Rose samples were collected from the gardens and greenhouse of FSC and used to extract RNA. Detection of PNRV and AMV was performed by RT-PCR. The results of the survey and what it means for the FSC rose collection will be discussed.

PP292 - Comparative Genomics of Transposable Elements in the Grasses

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Transposable elements (TE's) are the most abundant genetic loci found in eukaryotic genomes and often occupy more than 70% of the genome landscape. These genetic elements were first described in maize (*Zea mays*) and have been found in all eukaryotic genomes investigated. The grass family (Poaceae), has long been used as a model system to study transposable elements. Transposable element content has been mined in many grass species including, Maize, Sorghum (*Sorghum bicolor*), Sugarcane (*Saccharum officinarum*), Rice (*Oryza sativa*), and many others. This project aims to explore and characterize the repetitive elements in six grass genomes that are closely related to the grass tribe Andropogoneae, with the ultimate goal of better understanding the mechanisms that have driven the diversification of this important grass clade. Bioinformatic software Galaxy was used to identify and characterize the abundance of TE's in six novel grass species that have not been investigated to date. The presence/absences of specific TE's were then mapped onto a phylogeny of the Andropogoneae to better understand the dynamics of TE evolution. An improved understanding of repetitive elements across the grass phylogeny may uncover the mechanism behind the explosive evolutionary radiation of the grasses.

PP293 - Phylogenetic Resolution: Quantifying Variation in *Yucca flaccida*

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Yucca flaccida (Aiton) can be found across a broad range of habitats in Southeastern North America. This species is easily identified by its simple, unlobed leaves, showy white flowers, and tendency for the leaf margins to fray into threads. Morphological variation observed across its range and similarities with *Y. filamentosa* have led to taxonomic uncertainty. Based on our morphological observations, we hypothesize that *Y. flaccida* is a distinct species and that it is composed of two or more distinct morphological taxa. In order to test this hypothesis, we sampled 27 individuals across the range of North and South Carolina and sequenced two bar coding loci (rps16-trnQ, rpl32-trnL). Using this data, we have quantified genetic variation among individuals of *Y. flaccida*. Updates to the phylogeny of the *Yucca* genus are forthcoming.

PP294 - Characterization of BauF and its interaction with siderophore acinetobactin

Nathan Ikeda, William Penwell

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Acinetobacter baumannii is an ESKAPE pathogen, which means that it is resistant to most conventional antibiotics and can cause a wide range of serious infections in immunocompromised individuals. *A. baumannii* grows in varying conditions including iron-limiting conditions. The survival of this pathogen under these conditions is contingent on its acinetobactin-mediated iron acquisition system. This siderophore sequesters iron from the host but is dependent on other factors to cleave the siderophore and release the bound iron. Once released, the free iron is used for several metabolic processes. The BauF protein is postulated to be involved in the release of iron from the siderophore complex. Our goal is to further characterize BauF to determine if this enzyme is required for the release of iron from the siderophore-iron complex. To accomplish this goal, our first objective was to generate a *bauF* deficient strain by knocking out the gene. This allowed for the determination of a growth defect under iron limiting conditions. Future experiments will focus on the overexpression of the BauF protein and examining its interaction with the acinetobactin siderophore.

PP296 - Finding Phage: A Pursuit of Killers

Kaelyn Tyler, Gerard White

College Of Coastal Georgia, Brunswick, GA

SEA-PHAGES (Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science) is a two-semester, discovery-based undergraduate research course that provides students the opportunity to study bacteriophages ("phage"), environmentally ubiquitous viruses that infect bacteria. Although the most common biological entities on Earth and co-located with bacteria (e.g., marine/aquatic systems, soils, gastrointestinal tracts, etc.), phage are poorly understood. More research is needed to understand the basic biology of phage, their diversity, and their possible applications in medicine, agriculture, and industry. One goal of phage research is to isolate novel, lytic phage that will kill their bacterial hosts, with the intent of using phage when antibiotic treatments are unsuccessful for treatment of human infections due to development of antibiotic resistance. In this first semester of the SEA-PHAGES courses, the objectives are to: (i) isolate phage from soil samples; (ii) purify the phage to ensure clonal populations; (iii) amplify phage to obtain titers sufficient for electron microscopy and DNA extraction; (iv) submit DNA samples to The University of Pittsburgh (PITT) for sequencing; and (v) submit phage to PITT for archiving. PITT archives phages found through the SEA-PHAGES program and distributes samples when requested for

scientific use. Using host bacteria *Microbacterium foliorum* strain SEA B-24224, I isolated phage from soil (Fountain Lake Drive, Brunswick, GA). Phage samples have been submitted and I am currently awaiting results from electron microscopy. I feel that I have gained a better understanding of lab techniques, and research in general, through this program, and hope that I will use these in my future career.

PP297 - The Effect of *Allium Sativum*, Garlic, Oil on the Virulence Factor Alpha-hemolysin in *Escherichia coli*

Andrea Felix, Wanda Schroeder

Wesleyan College, Macon, GA

Essential oils are well known for their ability to protect plants against organisms such as bacteria, fungi, and yeast. In recent years, essential oils have become popular in humans as treatments for reducing stress, boosting immunity, curing headaches and aiding in digestion. The purpose of this study was to investigate the effect of a common essential oil, garlic oil, on the virulence factor alpha-hemolysin in *E. coli*. *E. coli* is part of the normal human digestive tract, but is also a common cause of urinary tract infections (UTIs), especially in elder adults. A previous study has shown that alpha-hemolysin in *E.* coli was not only able to lyse erythrocytes, but also nucleated host cells of the urinary tract. *E. coli* were incubated with varying concentrations of garlic oil and then plated on nutrient agar containing 5% sheep blood. The plates were incubated at 37°C for 24-48 hours and the zones of hemolysis were measured. The data suggested that garlic oil did not significantly affect the virulence factor alpha-hemolysin in *E. coli*.

PP298 - Prevalence of *Pseudomonas aeruginosa* in Central Kentucky waters

Braden Hatton

Midway University, Midway, KY

Pseudomonas aeruginosa is one organism in a large group of free-living bacteria that are said to be ubiquitous in the environment. *P. aeruginosa* is found in natural water such as lakes and rivers. This experiment evaluated the prevalence of *P. aeruginosa* in environmental water in the Central Kentucky area. Water samples were collected from different still and moving bodies of water and spread onto Pseudomonas Isolation Agar (PIA) plates to grow. Once colonies were observed, they were noted for distinctions and given Type names (e.g. Type 1). Each colony type was then plated on PIA for isolation. Amplification of target DNA was carried out by Polymerase Chain Reaction (PCR). Target DNA for *Pseudomonas* was 16s rDNA and for *Pseudomonas aeruginosa* was *rpoD*. Of the samples that have been tested, five were observed to be of *Pseudomonas* genus. Testing for *P. aeruginosa* of these five strains is currently being conducted. Once all samples have successfully undergone PCR, the prevalence of *Pseudomonas aeruginosa* in natural Central Kentucky waters will be identified.

PP299 - Association of filamentous nitrogen-fixing Cyanobacteria with *Oenothera humifusa* (evening primrose).

Emily Parker, Heather Joesting, Jennifer Brofft Bailey

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In nutrient poor substrates, such as sand, some plants compensate by association with nitrogen-fixing microbes. These microbes produce the enzyme nitrogenase, which catalyzes the reduction of N_2 to ammonia. Nitrogenase is encoded, in part, by the *nif*H gene. Because this gene is specific to nitrogen-fixing microbes, its detection in an environmental sample indicates the presence of this group. *Oenothera humifusa* (evening primrose) root samples (2 subsamples from 5 individuals) were collected from the dunes of Sapleo Island, GA (2015) and Tybee Island, GA (2016) as well as from Georgia Southern University, Armstrong campus in Savannah, GA (2017). DNA extracted from root samples was screened for the *nif*H gene by PCR. Amplified *nif*H genes were detected by gel electrophoresis, cloned, sequenced and analyzed. *nif*H sequences were aligned and pairwise compared; sequences having ≥ 95% nucleotide identity were grouped into an operational taxonomic unit (OTU). Among sampling locations, 93.3% of *Oenothera* individuals (n=15) tested positive for the presence of *nif*H. Collectively, 43 unique *nif*H sequence types (i.e., OTUs) have been identified (n=260 analyzed sequences). Based on BLAST comparison to GenBank sequences, 67% of these *nif*H OTUs (89.2% of *nif*H sequences) correspond to those of filamentous Cyanobacteria. The most common OTU (20% of *nif*H sequences) was detected in all locations and corresponded (97% nucleotide identity) to the filamentous cyanobacterial genus *Scytonema*. Collectively, the data suggests that *O. humifusa* roots from marine and non-marine habitats consistently associate with nitrogen-fixing Cyanobacteria. As a follow-up, we are currently testing (1) whether nitrogen-fixers also associate with above ground portions of *O. humifusa* (i.e., stems and leaves) and (2) whether the detected organisms are actively expressing *nif*H *in situ*.

PP300 - Characterizing the Cutaneous Microbiome of the Peaks of Otter Salamander in the Context of Infectious Disease

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In recent years, major declines in amphibian populations have been attributed to chytridiomycosis, a disease which has now been termed one of the deadliest diseases of all time. *Batrachochytrium dendrobatidis* (*Bd*), the fungus responsible for this disease, colonizes the skin of amphibians causing impaired osmoregulation and ultimately death. As the pathogen spreads globally, the disease has reached epidemic proportions. In wake of this, scientists are directing research to the antifungal properties of cutaneous microorganisms on amphibians as a possible defense against *Bd*. Certain bacteria, such as *Janthinobacterium lividum,* are known to produce molecules that inhibit this fungus. Harnessing this ability may serve as a possible solution to the present epidemic. The current study focuses on the microbiome of the Peaks of Otter salamander (*Plethodon hubrichti*) and the plausibility of its microbial symbionts functioning as potential antagonists to *Bd* growth in the species.

In the present study, the skin of thirteen *P. hubrichti* specimens collected from the Blue Ridge Mountains were swabbed. These microbiome samples were cultured on R2A plates and the individual microbial morphotypes were isolated. The DNA of each isolate was extracted, and the species were identified using 16sRNA gene sequencing. Then the metabolites of these microorganisms were isolated to produce Cell Free Supernatant (CFS). *Bd* was grown with these CFS samples in an *in vitro* challenge assay to assess the possible antifungal activity the metabolites have against *Bd.*

This study demonstrates the diversity of the cutaneous microbiome of *P. hubrichti*. Notably, bacteria belonging to the genera *Athrobacter*, *Bacillus*, and *Pseudomonas* were found present in the microbiome and are known to inhibit *Bd.* The in-vitro challenge assays results suggest various bacteria found in this microbiome inhibit Bd. These inhibitory microorganisms may serve as novel probiotics for affected amphibians or explain the severity of the infection in other species.

PP301 - Comparison of Lipid Extraction Yield between *Haematococcus Pluvialis* and *Chlorella Vulgaris*

Juan Morata, Elba Garcia, Maria Guillamont

Miami Dade College, Miami, FL

The growth and usage of photosynthetic organisms is a reliable source for biofuels. Its carbon footprint is almost nonexistent as a result of the photosynthetic process. Every day the global demand for sustainability increases, and the primary source of energy is now focusing on environmental protection. Several strains of microalgae have been selected as oil fuel alternatives (due to their ability to produce large amounts of biofuel) by oil and gas companies such as ExxonMobil. Additionally, the current top sources of energy are non-renewable while continuing to expand the ecological footprint. As per the United Nations summit of 2019, new environment-friendly techniques need to be adopted in order to ensure sustainability, and to reduce green-house gas emissions. The global community must enhance this behavior and would do so by relying on microalgae. *Haematococcus Pluvialis* and *Chlorella Vulgaris* are candidates to research a potential high-yield feedstock for biofuel production. This experiment was taken into consideration because of the availability and cost-efficiency of microalgae. Research suggests that these species can yield elevated levels of biomolecular substrates, lipids and carbohydrates. This study focuses particularly on the extraction of lipids after the cultivation of both strains of algae to determine which strain would be ideal for the creation of biofuel fuels.

PP302 - Cloacal microbiome composition of nesting loggerhead sea turtles using a non-culturing method.

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The proliferation of successful offspring is critical for the conservation and recovery of threatened species, such as loggerhead sea turtles. One threat facing embryos during clutch incubation is infection. Our research group has determined that unhatched loggerhead eggs on Georgia's barrier islands contain pathogenic microbes, most notably members of the *Fusarium solani* species complex (FSSC). Our long-term goal is to determine the degree to which these microbes are acquired from the mother's cloacal normal flora and from sand. We used a molecular approach to characterize the bacteria and fungi associated with the cloacal mucus of 17 loggerheads sampled over six nesting seasons. From extracted DNA, bacterial 16S rRNA genes and fungal internal transcribed spacer (ITS) regions were PCR amplified. PCR products were cloned, sequenced (via traditional Sanger sequencing), pairwise compared and grouped into operational taxonomic units (OTUs) based on 97% (bacteria) and 95% (fungal) nucleotide identity thresholds. The Ribosomal Database Project's Classifier software was used to assign each OTU the most specific taxonomic rank having bootstrap values of ≥ 80%. Preliminary screening of 9 turtles (167 ITS sequences) has not detected FSSC members thus far despite their common detection in unhatched loggerhead eggs using the same methodology, suggesting that the FSSC fungi originate from nesting sand. Among the 28 fungal OTUs recovered, only one was detected in multiple mothers whereas among the 67 bacterial OTUs (n= 198-16S sequences) analyzed thus far, 29.9% were recovered from multiple sea turtles and detected in other animal microbiome studies. The Proteobacteria, Bacteroidetes and Fusobacteria were the most commonly detected bacterial phyla and *Cetobacterium* were the most commonly detected bacterial genus. While the high diversity detected has prompted analysis by next generation sequencing, the data presented provides a baseline for study of microbes impacting incubating loggerhead eggs and of the loggerhead sea turtle microbiome.

PP303 - Characterization and Optimization of Biosurfactants Produced by Marine Bacterial Isolates

Chloe Baumgardner, Michelle Thomas

Campbell University, Buies Creek, NC

Biosurfactants produced by bacteria are structurally diverse amphipathic molecules that have potential as green alternatives to synthetic surfactants currently used in a myriad of industries. These natural molecules are biodegradable, versatile, and less toxic than synthetic surfactants. Biosurfactants interact with nonpolar and polar or charged compounds to lower surface and interfacial tension, which allows surface tension to be measured to detect changes in biosurfactant concentration. The aim of this project is to characterize the biosurfactants produced by marine bacterial species isolated from ocean invertebrates and optimize biosurfactant production through the alteration of growth conditions. It has been shown that biosurfactant production increases in the presence of an immiscible hydrocarbon; therefore, to encourage biosurfactant production, canola oil was added to the culture media. The surface tension of the whole cell culture was tested with a capillary surface tension apparatus in triplicate after 0, 48, and 144 hours of incubation. Characterized biosurfactant producers reduced surface tension with increased incubation time. Future studies will include growth condition optimization testing with various hydrocarbons and alteration of hydrocarbon concentration. Following the optimization of production, the biosurfactants will be extracted, purified, and structurally analyzed through thin-layer chromatography, infrared spectroscopy, and ^{1}H nuclear magnetic resonance.

PP304 - The microbiota in the canine gut of shelter dogs in relation to age, length of stay, and selected genetic factors

Katie Burelle, Kayla McCormick, David A. Johnson

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The microbiome of the canine gastrointestinal tract is essential to the overall health of individuals, playing an important role in nutrient absorption, protecting the host against pathogens, as well as other influencing other conditions. The goal of our study was to discover any correlations between the bacteria present in the canine gut and selected environmental and genetic factors. We used metagenomic DNA sequencing of a 16S ribosomal RNA segment to identify bacteria present in 20 shelter dogs. We found no clear correlation between either the length of stay or the dog's age and which bacteria were present. However, we did find that the diversity of bacterial genera decreased with length of stay. We also noticed that the occurrence of *Prevotella 9*, often found in the gut following a respiratory infection, shows an interesting pattern which may deserve further analysis. We also present preliminary results of correlations between specific canine disease-related alleles and the bacteria present.

PP305 - The Isolation and Annotation of Bacteriophages "MCubed" and "Nucci"

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Bacteriophages "Nucci" and "MCubed" were discovered during Queens' third year in the SEA-PHAGES program. As a part of the program, students at Queens work to research and discover new bacteriophages, viruses with the potential to fight bacterial disease and infections. Both phages were identified from soil samples collected from a chicken coop in Charlotte, NC. Using the bacterial host *Microbacterium foliorum* (*M. foliorum*), enriched isolation methods were used by students in the biology department to locate the presence of phage. Plaques from "Nucci" were clear, round, and typically less than 1 mm while "MCubed" displayed round, hazy plaques that were approximately 1mm. Transmission Electron Microscopy revealed that both phages exhibit the siphoviridae morphotype. After DNA extraction, the phages were sent to the Pittsburg Bacteriophage Institute for sequencing. Using the bioinformatics software DNA Master and resources HHpred, Starterator, Phamerator, and NCBI blastp, students annotated the genomes of "Nucci" and "MCubed". Both phages belong to the EA cluster, with "MCubed" being one of six phages in the EA2 subcluster and "Nucci" being one of two in subcluster EA10. "Nucci" contained 40,281 base pairs and a 63.7% Guanine-Cytosine (GC) content while "MCubed" contained 40,381 base pairs and a 62% GC content. Both genomes had 63 open-reading frames, with over half labeled as reverse genes. Following isolation, "MCubed" and "Nucci" were registered with the Actinobacteriophage Database, an online record of bacteriophages and their characteristics that is available for the public to view.

PP306 - Protocol for genetic transformation may differ for species of bacteria in the family *Enterobacteriaceae*

Kingsley Dunkley, Trey Doss

Abraham Baldwin Agricultural College, Tifton, GA

DNA transformation is a process that occurs naturally in bacteria by lateral and vertical transfer, altering genetic material by incorporating foreign DNA into each other's genome. This alteration is the cause of many mutations in different species of bacteria exporting fertility and resistant genes, for example, the increase in resistance of bacteria against antibiotics and expression of genes to produce metabolites such as enzymes. In biotechnology, DNA transformation is done artificially, once the DNA sequence is determined and the microbial molecular behavior and environmental factors are known. This process can be accomplished with appropriate procedures in a laboratory setting. The objective of this study was to determine if a specific heat shock and $CaCl_2$ DNA transformation protocol was successful for bacteria within the family Enterobacteriaceae. Protocol for DNA transfer for engineered *E. coli* was tested to ascertain the competency of *Salmonella* Typhimurium and *Shigella flexneri* for similar plasmid. Since most serotypes of *Salmonella* and *Shigella flexneri* are defective in metabolizing lactose, transferring a plasmid that expressed for beta-galactosidase gene was a novel approach. With basic adjustment to the protocol, preliminary results indicated that successful DNA transfer for species within the family Enterobacteriaceae may be eminent.

PP307 - Identification and characterization of oil degrading bacteria.

Annie Bright, Faith Steen, Michelle Thomas

Campbell University, Buies Creek, NC

We live in a world where oil is used extensively in daily activities. Crude oil is made into petroleum products which are used in a wide number of applications from automobiles, gasoline, to its by-products making plastic, polyurethane, and solvents. The pollution created from the use of crude oil can be minimized through bioremediation and identifying microorganisms that naturally metabolize and break-down hydrocarbons is crucial in steps toward a cleaner environment. For this project, bacteria were collected from oil and grease saturated soil and oil drip pan deposits from an automobile oil. Bacteria were isolated using enrichment broth containing Bushnell Haas Broth with motor oil as the only Carbon source. The morphology and Gram reaction of isolates were determined. Then, colony PCR was performed using 16S ribosomal RNA (rRNA) to identify the genus and species. To confirm the bacteria's ability to metabolize hydrocarbons, they were grown on four different growth media with differing combination of water, motor oil, and agar, against negative control which was without a hydrocarbon source. These results will further our research to explore the biochemistry behind their mechanisms to metabolize hydrocarbons. The increased discovery of microorganisms that can degrade hydrocarbons naturally will demonstrate the feasibility of bioremediation of oil and oil products.

PP308 - Potential Development of a Post-Mortem Interval Estimation using Microbiome Changes During Human Decomposition

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The process of human decomposition is highly variable and contingent upon numerous factors, including temperature, moisture availability, and insect and animal activities. While insects play a fundamental ecological role in decomposition and are often utilized for determining post-mortem interval (PMI), there are instances that limit their use. Likewise, microorganisms are vitally involved in the process of decomposition. Despite their vital role, research regarding microbiome succession during the decomposition process is limited, especially in superficial openings and cavities of the body. To further explore the relationship of microbes and decomposition, the microbiomes of the left ear and right nasal canals of six human cadavers in differing stages of decomposition in natural conditions in the environment were sampled. Whole genomic DNA was isolated using Qiagen PowerSoil Pro Kit with a modified protocol. We amplified the V4 region of the 16S rDNA gene using the 515F/1806R primers with 2X250 paired-end sequencing. Additionally, DNA samples were taken from soil and air for comparative purposes. A total of 28 million 16S rDNA sequences were generated using an Illumina sequencer with Next Gen techniques. Analysis of microbiome succession in the human decomposition process are discussed with an emphasis on the potential use of microorganisms as a forensic tool to determine time of death.

PP309 - Fungal Contaminants Isolated from Air Flow from the Ventilation System of an Elementary Classroom in Rural Alabama

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University of North Alabama, Florence, AL

Airborne fungal spores pose a health risk to many people, especially those that are considered sensitive due to allergies or respiratory diseases. One element of Sick Building Syndrome is fungal contamination of air vents and ductwork. In this study, agar was exposed to airflow at various points within an elementary school classroom that reported a high incidence of respiratory infections. Plates were grown 3-5 days at room temperature, samples were selected for isolation and subcultured onto fungal specific agar. Because several samples visually looked similar at the macroscopic level, a phase contrast microscope was used to investigate microscopic characteristics and group similar organisms for metabolic identification using the Biolog system. Information presented here reflects the diversity of fungi isolated from the elementary school classroom at the microscopic level.

PP310 - The Bacterial Pathogens on Spinach: Exposing the Dangers of the Common Leafy Green

Lindy Paffel, Annalyce Papo-Ramsey, William Penwell

Jacksonville University, Jacksonville, FL

Humans have developed a lethargic lifestyle in which they have become dependent upon the efficiency and convenience of commercial food products that provide simplicity in preparing healthy home-made meals. Common preparatory ingredients include the use of produce, specifically leafy greens such as spinach. Spinach is a nutrient-rich commercial food product with beneficial vitamins such as folic acid, dietary fiber, zinc, phosphorus and choline. Though spinach provides positive health benefits, recent reports from both the Center for Disease Control and Prevention (CDC) and the US Food and Drug Administration (FDA) have indicated the presence of pathogenic bacteria on the surface of spinach leaves including *Salmonella enterica*, *Listeria monocytogenes*, and *Escherichia coli*. The CDC indicated that 11% of all foodborne illnesses are derived from leafy greens such as spinach. In 2019, a recall of spinach was put into effect in 10 states due to the presence of pathogenic strains of *Salmonella enterica* that caused 200 illnesses and 4 deaths. To determine the identification of the bacteria, present on commercially available organic spinach, spinach samples were blended and cultured on nutrient and Rapid Enterobacteriaceae agar plates. Thus, accounting for the presence of both Gram-positive and Gram-negative bacterial species. Further analysis of speciation and populations will be identified through the use of MALDI-TOF MS. The ultimate goal of this research is to design a natural cleanser to combat the pathogenic bacteria that is found on spinach. Thereby decreasing the FDA approved number of harmful bacteria to ensure safety of consumption.

PP311 - MRSA Vice Versa: Intrusion of Community Acquired Methicillin-Resistant *Staphylococcus aureus* in a Healthcare Facility

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The University of Tennessee at Chattanooga, Chattanooga, TN

Methicillin resistant *Staphylococcus aureus* (MRSA) is a major threat to human health, notably in the healthcare setting. Due to its rapidly evolving antibiotic resistance and multitude of infection sites, MRSA has been associated with numerous outbreaks in healthcare facilities for over 50 years. The focus of this study was to perform molecular typing on MRSA samples collected from both patients and the environment in the neonatal intensive care unit (NICU) of a local healthcare facility. MRSA isolates were selected for using CHROM MRSA agar, and glycerol stocks were prepared for all candidates. For each isolate, genome extractions were performed prior to multiplex polymerase chain reaction (PCR) to determine the staphylococcal cassette chromosome *mec* (SCC*mec*) type of each MRSA sample. Identification of the SCC*mec* type allowed us to determine which sampling areas commonly harbored MRSA and whether the strain was healthcare-acquired (Types I, II, and II) or community-associated (Type IV and V). Our data revealed that a major portion of the suspected MRSA isolates were, in fact, Type IV (CA-MRSA). Specifically, we found CA-MRSA in the hospital setting through identification of Types IV and V in the environmental samples. In addition to Type IV, patient samples yielded Types I, II, and III (HA-MRSA). Taken together, the combination and overlap of MRSA types between patient and environmental samples raised concern about the cleaning regimens out-

sourced by the hospital. Our results informed the healthcare facility about the presence of MRSA, a major healthcare associated infection (HAI) causing pathogen in an ongoing process to improve cleaning procedures. Current studies are monitoring the effectiveness of the adopted protocols for reducing HAIs due to MRSA in this hospital.

PP312 - Coliform-specific Bacteriophages Isolated from the Intestinal Flora of Domestic Canines.

J. Spencer Campbell, Madison P. Owen, C. Brian Odom

Wingate University, Wingate, NC

Bacteriophages specific for coliforms were isolated from stool samples obtained from various domestic (pet) dogs. Lytic activities of these phages were also tested on various laboratory strains of *E. coli*.

PP313 - A candidate for Bacillus cereus phage therapy isolated from Wingate, NC soil

Kailey Ezekiel, Debra Davis

Wingate University, Wingate, NC

With the growing global concern of the antibiotic resistance crisis, alternative treatments methods, such as phage therapy, are being explored. *Bacillus cereus* is a human pathogen responsible for food poisoning found in commonly consumed foods. Phage usage has been proposed as a means of mitigating this problem either through treatment of the food products prior to consumption or as a remedy post infection. Phages and *Bacillus sp.* are ubiquitous in soil, which is an ideal source for phage isolation. Soil aseptically collected from the Wingate University campus was subjected to room temperature incubation with *B. cereus* host culture for phage selection and vacuum filtered using a 0.22 µm filter. This filtrate was combined with host culture and plated using the Top Agar method. Plaques with similar morphologies were collected and repeatedly amplified using the same plating technique. A phage deemed "BCP", though found to be effective against *B. cereus,* was tested to determine Firmicute host range including common antibiotic resistant species. BCP was ineffective against multiple *Staphylococcus* species, *B. subtilis,* and two previously characterized, antibiotic-producing *Bacillus* soil bacteria ("*78"* and *"79"*). The BCP phage may be a possible candidate for extremely targeted phage therapy, and therefore will be characterized through genome analysis. However, due to its limited host range, phage-resistance will be considered also. While a host may be resistant to a phage through mechanisms such as CRISPR, this is at the expense of other necessary functions and can result in a failure to thrive in optimal environments. This decrease in function may be monitored by exposing the phage-resistant bacteria to environmental and molecular stressors. The BCP phage-resistant *B. cereus* lysogens were developed and will be subjected to various environmental stressors including temperature and oxygen availability.

PP314 - Antimicrobial Applications of Defatted Hemp Byproduct Extracts

Julia Clements

Furman University, Greenville, SC

The legalization of agricultural hemp (*Cannabis sativa)* for production of cannabidiol (CBD) oil in the United States has opened up an industry centering around the benefits and uses of CBD. After hemp is pressed to release the oils within (defatted), the remains of the plant are discarded as byproduct. As the hemp industry continues to grow, more byproduct is being produced and discarded. This study aimed to explore the potential antimicrobial effects of extracts created from defatted hemp byproduct in different solvents such as acetone, methanol, ethanol and MAW (methanol:acetone:water 7:7:6). Extracts were tested using disk diffusion methods against *Bacillus cereus, Staphylococcus aureus, Pseudomonas aeruginosa, Salmonella typhimurium* and *Escherichia coli* and compared against the antibiotics penicillin and tetracycline. No extracts made using defatted hemp byproduct outperformed these antibiotics. While CBD oil may have multiple potential applications, there is little antimicrobial value in defatted hemp byproduct.

PP316 - Isolation, Identification and Characterization of Fermenting Wild Yeast Species From North West Georgia

Irma Santoro, Shawn Speight, Michael Arnold

Reinhardt University, Waleska, GA

Today many American craft breweries are experimenting with using alternative yeast or bacterial species to produce unique flavors and aromas in beers instead of using the domesticated strains of brewer's yeast, *Saccharomyces cerevisiae.* The aim of this study was to use morphological and molecular techniques to isolate, identify and characterize indigenous fermenting wild yeast species to produce novel, local beers with unique flavors. As a source of wild yeasts, various flowers as well as fruits and nuts from local trees were sampled on the Reinhardt University campus. Yeast colonies were isolated using malt/yeast extract/peptone/dextrose (MYPG) agar plates containing antibiotics and identified by colony morphology. As a result of the morphological analysis, six different yeast isolates were analyzed for growth, sporulation and the ability to ferment in different liquid medias (MYPG and barley-malt extract). Of the initial six isolates analyzed, four were chosen for molecular characterization using DNA barcoding techniques. The 5.8S rRNA gene was PCR amplified and sequenced to further identify the wild yeast isolates. The complete characterization of these wild yeasts will be reported. The ultimate goal of this study will be to identify novel wild yeasts that can be domesticated for use by the craft brewing industry. Through this project, we hope to use the possibility of brewing unique beers with our local craft-brewing partner, Reformation Brewery (Canton, Georgia) as an incentive to interest undergraduate students on either pursuing a mentored, independent research project or to pursue internship opportunities.

PP317 - Blue coloration in fungi: biochemistry, evolution, and functional ecology

Elizabeth Ragan, Nicole Hughes

High Point University, High Point, NC

The subject of adaptive coloration in plants represents an area of research that has blossomed over the last century; yet, adaptive coloration of fungi remains largely unexplored. The objective of the current study was to review the literature for information on the biochemical, evolutionary, and ecological basis for blue coloration in fungi. So far we have so documented blue coloration in 24 fungal genera, belonging to 18 families and 2 phyla. In some lineages, molecules responsible for imparting a blue hue are evolutionarily ancient (e.g. melanins and laccases), while in other lineages, blue molecules are unique to their family (e.g. xylindein- a quinone pigment produced solely by fungi in the genus Chlorociboria). In the vast majority of cases, however, the compound(s) directly responsible for blue coloration have yet to be isolated or described in the literature. In many taxa, differently-colored but structurally-related isomers and isozymes of the blue molecule occur within a species (most commonly white, yellow, or brown in color). In some cases, color change may be induced by changing media or growth conditions, but overall, it remains largely unknown why fungi would produce one colored molecule over another. Among the proposed functions of fungal pigments described in the literature include: protection from UV light, warming of sporocarps to create convection and disperse spores, and protection from host defenses. No studies have yet tested for beneficial effects of blue molecules specifically.

PP318 - West Virginia University Herbarium Digitization Projects

Matthew Sheik, Donna Ford-Werntz

West Virginia University, Morgantown, WV

This poster summarizes three recent digitization projects at the WVU Herbarium. The NSF "Keys to the Cabinet" digitizing and georeferencing grant, targeting 3 million specimens from across the southeastern U.S., concluded at the WVU Herbarium in June 2019. More than 92,000 plant collections in 223 families, 1314 genera and 4639 species from the 12-state region have been imaged and uploaded to the SERNEC portal. With the conclusion of this grant, the WVU Herbarium began work on two new projects. A multi-year U.S. Forest Service award was granted to support student labor for invasive plant research. The initial semesters of this project involved transcribing label data from WVU Herbarium records worldwide for seven species. Current work is focused on images from the iDigBio portal for *Arthraxon hispidus* and *Polygonum caespitosum*. The final project is a 3-year NSF funded Pteridophyte specimens grant. This is an award distributed to nine centers to digitize fern herbarium collections and fossils. The WVU Herbarium is participating through the digitization hub at the University of North Carolina, Chapel Hill. These projects demonstrate a sampling of digitization foci in taxonomy, floristics, and ecology.

PP319 - Digitizing the Raven Rock State Park Herbarium (RARO) in Central North Carolina

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Raven Rock State Park encompasses 4,810 acres along the Cape Fear River in Harnett County, North Carolina. The park is home to a small herbarium containing 305 specimens of the park's diverse flora. The majority of the specimens within the herbarium were collected from 1980 to 1995 by previous park personnel, Paul Hart and Mary Stevens. Recently, the herbarium has remained mostly untouched and had no database of which plants were represented by its specimens. In order to make the herbarium's contents available to the larger scientific community a digitization effort was initiated in the spring of 2019. During the summer of 2019, the herbarium was registered in Index Herbariorum with the code RARO. In August, the specimens were digitized by students and faculty at Campbell University using a digitization rig that was brought to the park by North Carolina State University faculty. Following digitization, specimen images were uploaded to the Southeast Regional Network of Expertise and Collections (SERNEC) portal. Specimen label data were captured throughout fall 2019. The herbarium was found to represent over 30 percent of the species previously documented within the park. RARO contains the largest number of digitized specimens from Raven Rock State Park and is therefore of relative importance in documenting the flora of North Carolina. Digitizing the herbarium allows the information that has been stored within the park for many years to be shared with the public on a much larger scale.

PP320 - Distribution and ecology of the Genus *Ilex* (Aquifoliaceae) in Mississippi

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Approximately 400 species comprise the cosmopolitan genus *Ilex* Linnaeus in the Aquifoliaceae. *Ilex* species are especially well-represented in tropical and temperate regions of the Americas and Asia. In Mississippi, there are 11 native and one introduced *Ilex* species based on herbarium records at collections within the state. The following currently recognized *Ilex* species have been documented in Mississippi: *I. ambigua, I. amelanchier, I. cassine, I. coriacea, I. cornuta, I. decidua, I. glabra, I. longipes, I. myrtifolia, I. opaca, I. verticillata,* and *I. vomitoria*. Some of these species, such as *I. decidua* and *I. opaca*, are widespread across Mississippi. *Ilex coriacea* and *I. glabra,* both primarily characteristic of acidic wetlands, and *I. vomitoria*, typically of upland sites, are common in the southern half of the state. The latter species appears to be expanding its range northward. Two species, *I. amelanchier*, and *I. cassine*, are of conservation concern and are restricted to wetlands in extreme southern Mississippi. The additional species *I. myrtifolia*, associated with pond cypress depressions and adjacent bay swamps, is also monitored by the Mississippi Natural Heritage Program. *Ilex cornuta*, native to Asia, is a naturalized part of the flora. From November, 2016 through November, 2018, *Ilex* specimens in the following herbaria were examined at their respective locations: University of Mississippi (MISS), Mississippi State University (MISSA), University of Southern Mississippi (USMS), Delta State University (DSC), Institute for Botanical Exploration (IBE), Mississippi Museum of Natural Science (MMNS), and the Southern Weed Science Laboratory (SWSL). Information on the distribution and habitats of *Ilex* species in Mississippi will be presented. This research

was partially supported by a Troy University Faculty Development Grant, by National Science Foundation grant DBI-1203687, and by the Mississippi Museum of Natural Science Foundation.

PP321 - Distribution and ecology of the Genus *Hypericum* (Hypericaceae) in Mississippi.

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An estimated 420 species have been recognized in the genus *Hypericum* A. L. de Jussieu in the Hypericaceae. *Hypericum* species are present on every continent except Antarctica. In Mississippi, 27 native and one introduced *Hypericum* species have been documented: *H. brachyphyllum, H. canadense, H. cistifolium, H. crux-andreae, H. denticulatum, H. drummondii, H. fasciculatum, H. frondosum, H. galioides, H. gentianoides, H. gymnanthum, H. hypericoides, H. lobocarpum, H. mutilum, H. myrtifolium, H. nudiflorum, H. perforatum, H. prolificum, H. pseudomaculatum, H. punctatum, H. setosum, H. sphaerocarpum, H. stragulum, H. suffruticosum, H. tubulosum, H. virgatum, H. virginicum,* and *H. walteri*. Of these, *H. myrtifolium* is on the state tracking list, and *H. nudiflorum* is on the state watch list. Habitats supporting populations of native *Hypericum* species include cypress swamps and marshes, frequently burned savannas and pitcher plant bogs, rich deciduous woodlands and adjacent meadows, prairies and chalk outcrops, and dry pinelands and sandhills. From November, 2016 through November, 2018, *Hypericum* specimens in the following herbaria were examined at their respective locations: University of Mississippi (MISS), Mississippi State University (MISSA), University of Southern Mississippi (USMS), Delta State University (DSC), Institute for Botanical Exploration (IBE), Mississippi Museum of Natural Science (MMNS), and the Southern Weed Science Laboratory (SWSL). Information on the distribution and habitats of *Hypericum* species in Mississippi will be presented. This research was partially supported by a Troy University Faculty Development Grant, by National Science Foundation grant DBI-1203687, and by the Mississippi Museum of Natural Science Foundation.

PP322 - Investigating Differences in Nutrient Dispersion through Contrasting Aquaponics Systems

This study examines differences in water quality and molecule dispersion in two different Aquaponics systems in Georgia Southern's SARC Greenhouse. Due to the difference in settles, where ammonia from each system's respective fish tank is converted to nitrate, the two systems can be expected to have observable distinctions in dispersion of nutrients as well as water quality parameters such as pH, dissolved oxygen and conductivity. Knowing how each settle affects the system will be useful for maximizing plant growth and creating more efficient renewable agricultural systems.

The data for this study was collected on a weekly basis, via the use of Vernier LabQuest water quality probes on samples collected from seven areas throughout both systems: One for the tank, one for the settle, four through the grow beds, and one for the sump. The parameters tested and recorded were ammonia, nitrate, potassium, pH, dissolved oxygen, and conductivity.

The Results showed that, where present, there was a steady decline in ammonia, dissolved oxygen, pH and potassium as the water traveled down both systems. The conductivity showed relative uniformity across both systems. For nitrate, the newer system one's nitrate levels had a tendency to gradually drop as the water traveled through, while system two's nitrate concentration had a tendency to be greater toward the end. This could suggest that system one's plants are gathering more nitrate as the water passes through, bringing them more nutrients and making the system more efficient overall.

PP323 - A study of endosperm developmental shift in Arabidopsis using the ectopic expression of InvINH1 by KRS promoter

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The endosperm and embryo are the result of double fertilization in flowering plants. Each structure has its own mechanisms for growth and development, but they rely on each other for successful seed development. In early stages of Arabidopsis seed development, the endosperm grows rapidly while the embryo grows slowly. After endosperm cellularization, this growth pattern changes so that the endosperm grows slowly while the embryo grows quickly. This shift in growth is likely due to nutrients shifting from the endosperm to the embryo. We hypothesized that invertase, an enzyme that breaks down sucrose, is one of the primary mechanisms for this nutrient shift. Invertase Inhibitor 1 (InvINH1) was identified in our lab as being specifically expressed before endosperm cellularization. Therefore, the presence of InvINH1 is correlated with slow embryo growth. To further investigate the effects of InvINH1 on embryo growth rate, KRS promoter was selected to ectopically express InvINH1 after endosperm cellularization. To construct the pKRS-InvINH1 chimeric gene, the coding region of InvINH1 was first amplified and cloned into a binary vector. Positive clones were verified by sequencing. Then, the 2048bp KRS promoter region was amplified from genomic DNA and cloned in front of InvINH1 coding region. This will allow us to express InvINH1 after endosperm cellularization. The 2048bp KRS promoter region was also cloned in front of a gene encoding the Green Fluorescent Protein, which will allow us to verify that KRS promoter is only active in cellularized endosperm. After the correct clones are verified by sequencing, the two constructs will be used to transform Arabidopsis plants via Agrobacterium-mediated floral dip method. For transgenic plants carrying the pKRS-InvINH1 transgene, we expect to see a delay in embryo growth, which will support our hypothesis that the function of InvINH1 is to suppress embryo growth before endosperm cellularization.

PP324 - Analysis of Phenolic Pigments in Neotropical Ericad Species

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The fruits of many Ericaceous species possess antioxidant anthocyanin compounds. Because of these antioxidant properties, anthocyanins have the potential to prevent cellular damage caused by reactive oxygen species. We have partnered with the Atlanta Botanical Gardens to extract and identify the anthocyanins from a number of neotropical Ericads. Whole fruit extracts will be prepared from samples obtained from plants of >40 Ericaceous plants from Central and South America. Analysis of the compounds will be done according to Dastmalchi et. al (2011) by comparing the absorbance of the extracts with a gallic acid standard curve. The phenols will be characterized using a mass spectrometer and screened for cytotoxicity against human triple-negative breast cancer cell lines (MDA 231 and MDA 468) and normal human breast epithelial cell line MCF10A.

PP325 - Evaluation of antiaging-like activity in tigernuts (Cyperus esculentus) and chili pepper (Capsicum annum)

Aging is a natural process of living organisms that consists of becoming older. In human and other animals, aging is accompanied by several physiological changes. These include deterioration and oxidation and wrinkles formation. Wrinkles formation may also be caused by various environmental factors such as excessive exposure to sun, pollution, and continuous deprivation of sleep. These environmental factors in turn cause oxidation of the skin cells and degradation of subcutaneous fatty acids, leading to the formation of wrinkles. Skin care and wrinkles treatment using pharmaceutical products are multi-million dollar industry. Plant based products are alternative methods for treating wrinkles of the skin or premature aging. Several antioxidants naturally found in plants have been associated with slowing or preventing wrinkle formation and premature skin aging. Tigernut (Cyperus esculentus) of the sedge family and chili pepper (Capsicum annum) of the nightshade family are two of the many plants mentioned in folk medicine to contain vitamins and enzymes necessary for skin care. The objectives of the study are to determine the antioxidant capacity of chili peper and tigernut bulb by analyzing their vitamins A, C, E contents. Tigernut bulbs and chili pepper fruits were extracted in distilled water and their vitamin A,E,C content analyzed. Preliminary data indicated that tigernut has more vitamin A and vitamin E contents than chili pepper but lower in vitamin C.

PP326 - The Effect of Host-Association on Stomatal Density of *Castilleja coccinea* (Orobanchaceae)

Sharon Spiess, Ben Gahagen

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Castilleja coccinea (Orobanchaceae), the scarlet Indian paintbrush, is an annual hemiparasite native to the prairies of the eastern United States. Hemiparasites are plants that can make their own food through photosynthesis while also taking nutrients from other plants via specialized, penetrating structures called haustoria. This host-parasite association establishes a direct connection between xylem tissues of both plants. The hemiparasite can then absorb water and minerals from the host xylem. Hemiparasites compete with their host by establishing a higher rate of transpiration in order to acquire the host's water and nutrients. There may be leaf developmental changes, concerning stomatal density, dependent on attachment versus no attachment to a host. This research will investigate and compare the stomatal density changes of *C. coccinea* when grown alone versus attached to a host, *Andropogon gerardii*.

PP327 - Ecophysiological Challenges Facing a Broadleaf Evergreen Angiosperm in Winter

Liliana Rangel-Parra, Hannah Houston, Megan Buzard, Howard Neufeld

Appalachian State University, Boone, NC

The southern Appalachian Mountains experience harsh winter conditions, including extremely cold air and soil temperatures, stochastic precipitation, often in the form of snow, high light, and strong winds. All of these contribute to the ecophysiological challenges that an evergreen plant faces during this season. Most wintertime research on evergreens has been done on conifers; we know less about how broadleaved angiosperms respond. Differences in leaf morphology between the two groups may influence mechanisms for coping with winter conditions. In addition, climate change is resulting in winters with stochastically dispersed warm days, and we do not know how broadleaved evergreens will respond to this. We are investigating the wintertime ecophysiology of the holly, *Ilex x* 'Nellie R. Stevens,' a broadleaved evergreen angiosperm commonly planted in this region. We are measuring diurnal gas exchange, water potential, maximum potential quantum efficiency (Fv/Fm), chlorophyll content, and leaf, soil, and air temperatures before, during, and after winter. We have found positive photosynthetic rates coupled with low stomatal conductances even at air temperatures slightly below or at 0°C, in part due to heating of the leaf above freezing when in full sun. Chlorophyll fluorescence measurements, however, indicate substantial photoinhibition for leaves exposed to high light at low temperatures, yet, they do not appear permanently injured and can achieve high rates on subsequent warmer days. Although rates are higher on warmer days in winter, cold soils may constrain the degree to which this species can take advantage of those days, due to the inability to transport water. Under sunny, winter conditions, low stomatal conductance may reduce latent heat loss, thus warming the broad leaves so they better cope with photoinhibition. This research can improve our understanding of how other broadleaf evergreen angiosperms may respond to natural as well as anthropogenically-influenced seasonal trends.

PP328 - Investigating the Influence of Volatile Chemical Cues in Foraging Behavior of the Rare Parasitic Plant *Cuscuta harperi*

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Cuscuta is a large genus of stem-parasitic annual vines. Some *Cuscuta* species are capable of parasitizing numerous hosts while others exhibit a higher degree of host specificity. *Cuscuta* species are obligate holoparasites due to their ultimate dependence on locating and attaching to host plants for survival and completion of the life cycle. Research has shown that at least one species of *Cuscuta* can detect volatile organic compounds (VOCs) emitted by potential host plants and use them as chemical cues for directional growth during foraging.

Harper's Dodder (*Cuscuta harperi*) parasitizes only a few host species within its narrow geographic range and is potentially vulnerable to extinction due to habitat and host specificity, small population size, and threats of habitat destruction. Little is known about specific cues used by *C. harperi* to initially locate a host. We hypothesize that *C. harperi* uses VOCs to detect the location of potential host plants and that similar patterns of chemotaxis seen in a weedy, generalist species of *Cuscuta* will be observed during foraging of *C. harperi* seedlings. To address this hypothesis, we placed newly germinated seedlings in proximity to a living host plant and a control pot of soil to monitor foraging behavior in the first 48 hours post-germination. We expect seedlings to grow nonrandomly in the direction of a VOC concentration gradient produced by a suitable host in the absence of light cues.

Elucidating the mechanisms underpinning foraging behavior in *C. harperi*, could allow us to demonstrate that the ability to sense and respond to VOCs is not unique to weedy species, but rather that this ability is shared by host-specialist and generalist species alike. Advancing our understanding of the physiology behind host-parasite interactions has the potential to inform strategies for control of weedy species of *Cuscuta*.

PP329 - Examining morphological and habitat variation within *Stenanthium gramineum* (Eastern Featherbells, Melanthiaceae)

Hannah Cook

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The perennial herb *Stenanthium gramineum* (Ker. Gawler) Morong, or "Eastern Featherbells" occurs in the Southern Appalachians and more broadly throughout the midwestern, southwestern and eastern U.S. Two varieties are distinguished partially by habitat differences: *Stenanthium gramineum* var. *gramineum* occurs on rock-outcrops, grassy balds, and serpentine barrens. *Stenanthium gramineum* var. *robustum* (S. Watson) Fernald is found in bogs and wet meadows; it is listed as endangered and threatened throughout its native range of the eastern U.S. A third variety, *S. gramineum* var. *micranthum* Fernald, is not currently recognized, but was described on the basis of its unique granitic dome rock outcrop habitat. I investigated morphological and ecological characteristics of the three *S. gramineum* varieties in order to clarify their taxonomy and aid conservation. Morphological and environmental variables such as plant height, phenology, soil pH, and soil depth were measured in seven flowering populations of var. *gramineum* and var. *robustum* in summer and fall, 2019, and samples were collected for morphological, leaf anatomical, and pollen analysis. In addition, multiple morphological characters were measured on herbarium specimens from throughout the ranges of each taxon. Multivariate analyses were performed to determine whether two or more distinct entities could be discriminated based on these data. This study has aided in the clarification of the taxonomic status of *S. gramineum* varieties and has determined the most reliable characters used to define them. Furthermore, it should facilitate identification of these taxon and conservation of the rare var. *robustum*. No field populations of var. micranthum were located, and few herbarium specimens that agreed with this taxon were observed.

PP330 - Characterizing growth, stress, and CBD content in three varieties of hemp, *Cannabis sativa*

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Recent legalization of *Cannabis sativa* cultivation for fiber and medicine has opened new doorways for research on this fascinating plant. The objective of this study was to compare growth, mortality, cannabidiol (CBD), tetrahydrocannabinol (THC), and physiological stress (measured as Fv/Fm) in three cultivars of *Cannabis sativa,* in order to determine which varieties are optimal to grow in the piedmont of North Carolina. The three hemp varieties we studied were: Cherry blossom, Baox, and Cherry wine. Between 141-159 cloned plants of each type were transplanted into an agricultural field fitted with drip irrigation in Mocksville, NC in May 2019, and harvested in September 2019. Pre-dawn Fv/Fm (maximum quantum yield efficiency of photosystem II) was measured once every two weeks for ten randomly-positioned plants of each variety. Following harvest, these same plants were dried, and total above-ground biomass and height were measured. CBD and THC content were determined using using LC-MS the week before harvest. CBD content was highest in Baox (12%), which was nearly double the CBD content in Cherry wine and Cherry blossom (5.9 and 6.9% respectively). The CBD:THC ratio was also highest in Baox (48:1), followed by Cherry blossom (34:1) and Cherry wine (14:1); in all samples, THC was at or below 0.25% (federal limit being 0.3%). Total plant biomass, height, and Fv/Fm were statistically similar between the three cultivars. All varieties were relatively successful (<10% mortality), but survivorship was greatest (<5% mortality) in Baox. While our results admittedly lack adequate replication due to continuous planting design, we tentatively conclude that higher CBD content and CBD:THC ratios in Baox, combined with greater survivorship, may render it more desirable as a CBD crop in this region than the other varieties tested.

PP331 - Effect of light and leaf age on the pigment composition and gas exchange characteristics of *Croton petra*, a shrub with multi-colored leaves

Regina Javier, Alexander Gustafson, Howard Neufeld

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Croton petra is an ornamental shrub native to Indonesia, Malaysia, Australia, the Western Pacific Ocean islands and India which displays yellow, red, green, and purple on its leaves. We characterized the progression and pattern of color change from young to old leaves on three *Croton petra* plants. Young leaves are typically yellow, containing little or no chlorophyll. As leaves age, they produce more chlorophyll, carotenoids, and anthocyanins. Leaves first start out yellow, then transition to green, after which they turn orange, then red, before finally ending a deep purple. The variations in the colors of *Croton petra* throughout its development have not been well studied, but seem to suggest that as leaves age, they become more sensitive to high light and these leaf pigments might act to protect leaves from high light stress. We measured photosynthesis at saturating light in leaves of varying colors using the Li-6800 gas exchange system. Rates were negative in the youngest, red leaves (-0.2 μmol m^{-2} s^{-1}), and increased with leaf age for dark green leaves with yellow veins (0.6 μmol m^{-2} s^{-1}) to dark green leaves with red veins (2.1 μmol m^{-2} s^{-1}). Rates of stomatal conductance paralleled those for photosynthesis. To determine how light intensity may affect pigment production, plants will be grown under varying light conditions of full sun, 50%, and 90% shade. Rates of photosynthesis and pigment levels will be determined for young and old leaves for plants in each of these light treatments. Light and CO_2 response curves will be done to determine how age affects responses to these parameters. We will also test our light stress hypothesis by exposing differently aged leaves to 2 hours of high light and measuring Fv/Fm from chlorophyll fluorescence, a measure of the integrity of PS II.

PP332 - Neighborhood Effects on Physiology of Turkey Oak (*Quercus laevis*) Seedlings in a Longleaf Pine (*Pinus palustris*) Ecosystem

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Changes in climate place new stresses on forest ecosystems, thereby complicating management plans. The Adaptive Silviculture for Climate Change (ASCC) project develops and evaluates forest management strategies designed to encourage tolerance to such changes. At a longleaf pine (*P. palustris* Mill.) dominant site in southwestern Georgia, the focus is on tolerance to drought, an increasingly important climatological feature of the southeastern United States. The 'transition' strategy at this site aims to develop a forest in equilibrium with a hotter and drier climate, using overstory density reduction and seedling plantings to reduce water stress and shift the hardwood component of the forest towards more drought-tolerant species, including turkey oak (*Quercus laevis* Walt.). This study addresses the feasibility of regenerating *Q. laevis* in a *P. palustris* ecosystem and examines seedling performance in relation to planting location. Seedling leaf gas exchange and microenvironment were measured over one growing season, and examined in relation to overstory metrics for indications of competition and facilitation. Leaf net photosynthetic rate responded positively to increases in photosynthetically active radiation (PAR), soil volumetric water content (VWC), and canopy openness. Stomatal conductance responded positively to increases in VWC and canopy openness, and to decreases in vapor pressure deficit (VPD). PAR and VPD were not significantly affected by any overstory metrics, while VWC responded negatively to increasing *P. palustris* overstory abundance index. Results suggest that *Q. laevis* seedlings are well adapted to drought conditions at the site. However, seedling leaf physiological performance was negatively impacted by the overstory, with little evidence of facilitation. Efforts to transition the *P. palustris* ecosystem towards greater drought tolerance may therefore be most effective when the planting of *Q. laevis* seedlings is concentrated in canopy openings. Such improvements in management efforts are valuable to managers of this highly biodiverse ecosystem in preparing for climate change effects.

PP333 - An Analysis of Vessel Elements and Theoretical Hydraulic Conductivity of *Solidago altissima* Stems

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The hydraulic conductivity (K_h) of a plant depends on the diameter distribution of vessels, porosity and density of pit pores in the sidewalls that allow vessel-to-vessel transport, vessel length, and number of vessels in the stem. The Haagen-Poiseuille Law (HPL) states that volumetric flow-rate through a circular vessel is proportional to the fourth power of vessel radii, meaning a small increase in radius yields large increases in flow. The research reported herein was part of a physiological study on three cytotypes of goldenrods (*S. altissima*) that includes eastern (EH) and midwestern (MH) hexaploids and midwestern (MD) diploids. Since polyploids often have larger cells than diploids, we undertook a study to determine whether theoretical K_h would be higher in the hexaploids. Stem cross sections were taken from 5 individuals/cytotype, 1m above their base. To assess vessel size, we measured the major and minor axes and area of 50 vessels within a single ray/plant, and % vessel area within a randomly chosen 0.04 mm^2 area. We used a modified form of HPL that adjusted flow for elliptically shaped cells, since most xylem cells were noncircular, and such cells have lower flowrates than circular ones. We summed all 50 cells to obtain a stem K_h for each cytotype. K_h was highest in EH (5.53×10^{-10} m^3/s), followed by MD (2.78×10^{-10} m^3/s) and MH (2.08×10^{-10} m^3/s). Very large vessels in EH, some 2x the area of the largest vessels in MH and MD, contributed greatly to the high EH flow-rate. Curiously, the largest differences in K_h were between the two hexaploids, which mirrors a similar difference in gas exchange from another study of ours, where photosynthesis and stomatal conductances were higher in MH than EH. We plan to conduct further studies to elucidate the relationships between polyploidy, K_h and gas exchange.

PP334 - Longleaf pine seedling physiology: a tale of two soils

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Longleaf pine (*Pinus palustris* Mill.) exhibits a unique form as a seedling delaying stem growth for up to 10 or more years. In this so called "grass-stage" the seedling grows a taproot sometimes up to a meter long. Keeping its meristem at soil level offers protection from the frequent fires that occur in the system while the taproot allows for water access and starch storage for re-flushing of needles post-fire. With renewed interest in reforestation across its former range, understanding seedling-level physiology will be crucial in successful restoration efforts. Under our changing climate, it is important to record current variation in physiological adjustments the seedlings make under different environmental conditions to predict what might happen in the future. This study aims to understand adjustments that grass-stage longleaf seedlings make on different soil types.

Gas exchange and leaf water potentials were measured during the summer of 2019 on seedlings on two soil types of different drainage classes (sandy and loamy sand). Differences between sites were expected based on the water-holding capacities of these two soils and were reflected in the differences in mid-day water potentials at each site. During a drought in mid-September, pre-dawn water potentials were much lower on the sandy site. Gas exchange varied slightly between sites especially time of day when maximum stomatal conductance was reached. Seedlings from each site were excavated and the following measurements taken on the whole seedling: bulk leaf xylem water flow, stem flow and root flow. Partitioning these data helps us understand the where the hydraulic resistors might be in the path water takes from the roots to the atmosphere through the seedlings. In knowing the plant's water status along the continuum, we can better monitor regeneration conditions and make informed decisions as we continue to restore this tree across its range.

PP335 - Assessment of a fluorescence microscopy and mammalian cell culture CURE with an underrepresented STEM student population

Jennifer Hurst-Kennedy, Michael Saum, Cindy Achat-Mendes, Allison D'Costa, Elisabeth Javazon, Shoshana Katzman, Ernest Ricks, Jr., Alessandra Barrera

Georgia Gwinnett College, Lawrenceville, GA

Georgia Gwinnett College (GGC) is an access institution with a diverse student body, located in metro Atlanta. To strengthen research skills, teach employer-valued cell biology laboratory techniques, and increase student engagement; a semester-long, inquiry-based CURE was developed and implemented in Cell Biology with Laboratory (BIOL3400K), a sophomore-level course, which serves as a "gateway" to all upper-level Biology courses. This CURE centers on the investigation of a student-chosen experimental factor on the viability of cultured, mammalian cells. Through participation in this CURE, students gain experience in cell culture, fluorescence microscopy, and viability assays, and strengthen important research skills, such as literature searches, graphing, and data analyses. The impact of this CURE on student learning gains and attitudes was assessed using a pre-/post- content exams and the Colorado Learning Attitudes about Science Survey (CLASS). Our data show that all students made significant content gains. Female students made larger learning gains than male students. Additionally, minority students performed better than majority students in some content areas. Student attitudes did not change, or in some cases were slightly more negative after the CURE. Overall, this CURE had a positive impact on students by engaging them in an inquiry-based laboratory experience.

PP336 - A CURE for the Behavioral Endocrinology Classroom

Danielle Satre

Reinhardt University, Waleska, GA

Research experience is vital to an undergraduate seeking a degree in Biology as it provides a much deeper level of understanding as to what science is and how the process of science works. However, unfortunately, many students do not get the opportunity to do research as an undergraduate, especially at small schools that are not equipped to make these experiences widely available. At many small institutions it is often the case that there are not enough faculty in a department to lead a large number of majors through independent research projects. One remedy for this issue is to develop CUREs (course undergraduate research experiences) for use in undergraduate classes. Utilizing CUREs enables the faculty member to lead groups of students through the development and implementation of a full research project.

A CURE for use in a Behavioral Endocrinology course was developed in order to increase student understanding of research in Biology as well as to reinforce the material students were learning in the course. Students were given a few initial guidelines and then spent lab periods and time outside of class developing and carrying out a research project. Students brainstormed to develop their idea, reviewed current literature and participated in online discussion groups in which they shared various articles they had found, and discussed further development of their hypothesis and predictions. They then planned the experimental design and applied for approval from the Institutional Review Board. Upon approval, students carried out their project, analyzed their data independently, and wrote individual lab reports to share their findings. In doing this, students reported that they had a better understanding of the scientific method, how to identify and utilize scientific literature, develop and carry out an experiment, and for the first time in their undergraduate career, "they felt like scientists".

PP337 - Using Learning Assistants to Enhance Student Outcomes in CUREs Courses

Ann Showalter, Barbara Musolf

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To address retention and student success challenges, we have recently transformed our major's introductory biology laboratory courses using the course-embedded undergraduate research model (CURE) that emphasizes experimental design and data analysis skills. To support student learning in our CUREs laboratory courses, we created a learning assistant program, in which an experienced student is imbedded in each lab section. Learning assistants receive training in pedagogy to enhance their abilities to assist students. In lab, learning assistants answer questions and facilitate trouble-shooting of experimental design and data analysis. Additionally, learning assistants hold regular office hours, during which students can get assistance with assignments that require practicing the skills they learn in lab. We have found that the number of visits to these office hours is positively correlated with student exam scores in lab. Perhaps more importantly, learning assistants improved student skills requiring higher-order thinking and helped students feel more integrated into the biology department.

PP338 - A curriculum embedded undergraduate research experience that utilizes the antlion (Family Myrmeleontidae) feeding and behavior

Patrick Cain, Mark Schlueter

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Here we present our experiences developing a CURE project that utilizes antlions. Antlions are insects in the Family Myrmeleontidae and are best known for the fierce prey-capturing behavior exhibited by their larvae. The main goal of the following proposal is to create a CURE project that utilizes antlions in the introductory BIOL 1108K course to help increase student engagement. In this project, we introduced BIOL 1108 students to the biology and behavior of antlions. The specific focus of the project initially was the predatory behaviors and feeding habits of the antlion larvae. Students in each class were divided into groups of three or four to complete the initial project, after which the students developed a second experiment of their own design. We compared survey data covering basic biology, experimental design, and antlion biology between three BIOL 1108 sections that used antlions and two sections that conducted corn growth experiments (control groups). BIOL 1108K has three STEM skills assigned to it (data analysis, effective communication, ability to apply evolutionary concepts). Thus, during this research project, students gathered raw data in their experiments and then used t-tests and ANOVA to compare, contrast, and interpret data. Students also practiced their "effective communication" by writing a scientific paper. Evolutionary concepts will be explored, discussing the ecology and evolutionary principles behind the predatory tactics of the antlion larvae. While antlions are generally easy to work with, observing predatory behavior is always challenging.

PP339 - Course-embedded Undergraduate Research Experiences: CUREs for closing the performance gap in under-prepared and under-represented groups in STEM fields

Clay Runck, Judy Awong-Taylor, Allison D'Costa, Tirza Leader, Cindy Achat-Mendes, Chantelle Anfuso, David Pursell

Georgia Gwinnett College, Lawrenceville, GA

The School of Science and Technology at Georgia Gwinnet College has incorporated Course-embedded Undergraduate Research Experiences (CUREs) for the past 8 years as part of a comprehensive systems approach model to transform STEM learning, student engagement, and inclusivity for our student population. Central to our model is the growing body of evidence that shows a link between student research and lasting learning, and that research experiences increase students' interest in careers in STEM. Incorporating multiple CUREs throughout all four years of matriculation for all STEM majors provides a mechanism for successfully engaging large numbers of students in undergraduate research and provide them with the skills and confidence to seek out independent, faculty-mentored research or alternative summer research opportunities. Results from an on-going, in-depth study that currently includes 2 years (4 semesters) of quantitative and qualitative assessment data on the impact of CUREs on student success and engagement, including impact on ethnicity, gender, course grades, and student attitudes show: (1) CUREs have led to a more positive belief in self-efficacy for all questions pertaining to communication, experimental design, career choices, and critical thinking/problem solving; (2) an emerging trend for course grades to be higher in CURE sections versus controls in biology and chemistry but not math and Information technology; and (3) no significant effect of CUREs on mean course grade for any race except for African Americans. Taken together, our current data suggest that CUREs, a High Impact Practice, may be helping to close the performance gap in under-prepared and under-represented groups in STEM fields. Successes and challenges of implementing our CURE model at Georgia Gwinnett College, an open access institution with a highly diverse population of students, including many from groups traditionally underrepresented in STEM education, will also be presented.

PP340 - A CURE for Biotechnology Labs to Identify Genetically Modified Foods

Ernest Ricks, Jr., Cindy Achat-Mendes, Jennifer Hurst-Kennedy, Robert Haining

Georgia Gwinnett College, Lawrenceville, GA

This CURE provides students the opportunity to learn and use leading techniques in biotechnology, while strengthening their understanding of the central dogma of biology, and facilitating an authentic research experience. In one module, students can use PCR to detect the presence of common genes found in genetically modified (GM) foods. In a second module, students can isolate messenger RNA, synthesize cDNA, and employ real-time quantitative PCR to investigate the expression of GMO genes. The last module utilizes Enzyme-Linked Immunosorbent Assay (ELISA) to detect the presence of GM proteins. Students receive training in lab research/STEM skills including troubleshooting equipment, experimental design, maintaining a lab notebook, writing manuscript-style lab reports, and oral presentation of research findings. Students are required to know the purpose of reagents and procedures rather than follow cookie-cutter

recipes. They learn the theory and application of PCR, real-time PCR, and ELISA to investigate the relationship between genes, RNA and proteins, respectively, in GM foods. This CURE resulted in over 20 campus and regional conference student presentations over the past 3 years. The effectiveness of this project was assessed by evaluating gains in *student learning and student attitudes* towards research and STEM careers. Assessment tools included: *a) pre- and post- content surveys* (multiple choice questions that are linked to course learning objectives), *b) 4-year URE student survey*, and *c) Lab report rubric designed by the Biology Faculty.* The attitudinal survey data suggest that following participation in the GM foods lab design students: 1) Became more knowledgeable about the testing of genetically modified foods and central dogma; 2) Appreciated designing and taking ownership of their own research project; 3) Expressed better understanding of research in the biotechnology field. Significant outcomes of this new lab curriculum include student-initiated hypothesis-driven authentic research projects, troubleshooting and critical thinking as students worked through technical challenges.

PP341 - Assessing Experimental design, a valuable STEM skill, in an Introductory Biology course.

Allison D'Costa, Cindy Achat-Mendes, Candace Timpte, Judy Awong-Taylor, Latanya Hammonds-Odie, Pat Uelmen Huey, Elizabeth Javazon, Joshua Edwards, Tirza Leader

Georgia Gwinnett College, Lawrenceville, GA

The Principles of Biology I, BIOL1107K labs have been redesigned with a course-embedded undergraduate research experience (CURE) to provide *multiple* opportunities for students to learn and practice experimental design, a valuable STEM skill. As part of the CURE, students conducted in-depth investigations on two topics: (a) effect of UV radiation on yeast survival, and (b) enzymatic reactions and factors affecting enzyme activity. Using guided inquiry and minimal handouts, students had at least three opportunities to design controlled experiments iteratively. "Control" lab sections followed a traditional lab manual that provides step-by-step style instruction, and students had only one opportunity to design a controlled experiment. A validated Experimental Design Ability Test (EDAT) was administered as a pre-test during the first week of the semester, and a post-test at the end of the semester. At the end of the semester, students' pre and post-tests were graded by two faculty members using a validated rubric. To prevent bias in grading, a blind study was developed in which two different versions of the EDAT were created. For students in each course section, either version of the EDAT was administered as pre or post assessments by a person not affiliated with the course. Lessons learned, effectiveness of the assessment instrument, data analysis comparing control and CURE sections, as well as the impact of the CURE on building the targeted skill, will be discussed.

PP342 - Transforming Traditional Biology Labs: Quantitative Analysis of Organic Molecules in Plant-derived Foods

Xiaorong Zhang, Andrea L. Moore, Takayuki Nitta, Andrew Methven

Savannah State University, Savannah, GA

The CURE team at Savannah State University designed and implemented a CURE project that transformed the traditional Organic Molecules lab into a hypothesis-driven mini-research project in the BIOL 1107L – Principles of Biology I Lab, focusing on STEM skills. Students used Scientific Method throughout their research, from generating a hypothesis and designing an experiment to analyzing data and making a conclusion. The CURE team assessed students' skills in experimental design and data analysis through several approaches, including the Experimental Design Ability Test (EDAT), lab reports, and questions on the lab exam. The EDAT was performed as a pre- and post-test to measure student improvement in experimental design. All assessments were conducted for both non-CURE group (control) and CURE group to measure the potential impact of the project on student learning.

PP343 - Optimizing Algal Growth: A CURE for your Curriculum

Andrea L. Moore, Xiaorong Zhang, Takayuki Nitta, Andrew Methven

Savannah State University, Savannah, GA

As a part of the Vision and Change movement, a team of biology faculty at Savannah State University have begun to redesign the introductory biology labs to include a component where students apply the process of science through CUREs. The team has developed and implemented a CURE entitled, "Photosynthesis: Algal Growth Experimentation," which is a modification of "Algae to Energy: Optimizing Systems" lab by Boyce Thompson Institute. The CURE answers questions about alternative energy sources and allows student to manipulate variables to optimize algae growth. This CURE is a great addition to your toolbox and can be easily integrated into a pre-existing course or scaled up to full semester projects. A description of the CUREs, STEM skills, and ideas for scaling are provided here.

PP344 - Microbial diversity in a "Pond in a Jar" ecosystem-A CURE at the University of Louisiana Monroe

Chris Gissendanner, Tom Sasek, Srinivas Garlapati, Timothy McMahan

University of Louisiana Monroe, Monroe, LA

Microbial diversity is an important component of all ecosystems. In humans, disruption of the microbial ecosystem of the gut can lead to serious health consequences. We have designed a CURE that investigates the effects of environmental disruption on the microbial diversity of a laboratory "pond" ecosystem. This CURE is an update of a "Pond in a Jar" project that has been a part of the introductory biology lab course at ULM for over 15 years. In the updated CURE, students utilize microbiological techniques to quantitatively and qualitatively assess microbial diversity following chemical disruption of the ecosystem. We intend for this CURE to address the following STEM skills: 1) Ability to apply the process of science; 2) Scientific communication; and 3) Data analysis. Experience from the initial implementation of the CURE led to revisions to better guide students in quantitative analysis and interpretation of results. The current version also incorporates identification of bacteria by 16S rDNA sequencing. We will present the results of this ongoing effort.

PP345 - Implementing CUREs in the Curriculum: Results of Experimental Design Ability Test (EDAT)

Andrea L. Moore, Takayuki Nitta, Xiaorong Zhang, Andrew Methven

Savannah State University, Savannah, GA

As a part of the Vision and Change movement, a team of biology faculty at Savannah State University have begun to redesign the introductory biology labs to include a component where students apply the process of science through CUREs. The team has developed and implemented two CUREs that transform the traditional cookbook labs into two short mini-research projects designed to answer real world questions. The first, Quantitative Analysis of Organic Molecules in Foods and the second CURE entitled, Photosynthesis: Algal Growth Experimentation, are aligned to the student learning outcomes for the lecture class and provide skills that will be used in successive courses. The organic molecules CURE allows students to measure the protein and carbohydrate concentration of foods to address the claim that vegans can get the necessary components for a healthy diet. The photosynthesis CURE is a modification of Algae to Energy: Optimizing Systems lab by Boyce Thompson Institute and allows students to manipulate variables (CO_2 or wavelength of light) to optimize the growth of *Chlorella*. The CUREs allow students to apply the scientific process, analyze data, and write for the sciences. We assessed students' ability to apply the process of science by designing experiments. The Experimental Design Ability Test (EDAT) was administered as a pre- and post-test with one formative assessment for the CURE sections. Results of the first two years of implementation, challenges, and concerns will be shared.

PP346 - Cannabidiol and Cancer: Adventures from Cell Biology

Ruby Thamert, Emma Schaffer, Andrew Kirk, Lori Hensley

Jacksonville State University, Jacksonville, AL

Students in cell biology lab used resources from the Cell Biology Education Consortium to design semester-long research projects in their course-based lab. For this project, students chose to test the effects of commercially available cannabidiol (CBD) oil on viability and metastatic potential of breast cancer, Ewing's sarcoma and melanoma cell lines *in vitro*. MTT and transwell migration assays were performed to test and compare the effects of a medically reputable CBD oil, a hemp elixir from the Forbes top twenty list of CBD products, and a CBD-containing drink from a local gas station on these cell lines. Data demonstrate a dose-dependent effect on both cell viability and migration in all cell lines with the medically-reputable oil. The hemp elixir and CBD drink were only tested with breast cancer cells. The hemp elixir also demonstrated dose-dependent effects on both viability and migration, while the CBD product from the local gas station had no effect on either of these hallmark characteristics of cancer cells. These results suggest that all CBD products may not have equivalent medicinal value and that some over-the-counter CBD products are effective in decreasing cell viability and the metastatic potential of various cancer cell lines in a dose-dependent manner, which prompts the need for more intensive studies on the topic.

PP347 - Leveraging CUREs and CBEC Educational Resources to Provide Students Access to Education Based Research

LaShall Bates

NorthWest Arkansas Community College, Bentonville, AR

The opportunities for students to design and implement a scientific research project are limited at a community college. The Cell Biology Educational Consortium (CBEC) assists faculty in developing and implementing CUREs in the classroom. One of the key focus areas for CBEC is to provide access to cell-culture based research to undergraduates at any level. Using CBEC as a resource, a cell culture laboratory was initiated at NorthWest Arkansas Community College (NWACC) supporting multiple educational experiences. Support from CBEC provided a platform to educate faculty and administrators to the advantage of providing scientific research opportunities involving cell culture to community college students and helped in securing additional funds to outfit the lab space. Initially students in Cell Biology had the opportunity to design and implement a research project using U87 mammalian cells. Students in Anatomy and Physiology, Gen Bio, Genetics, and Zoology were also able to observe the cells as part of their courses. The initiation of the lab had a broad impact across the Science department. In the courses, the student's control over the design and implementation of the project led to increased understanding of science and experimentation.

PP348 - The Efficacy of Cannabidiol and AKT-i as Cell Proliferation Inhibitors

Zane Smith[1], Timothy Spiva[1], Nathan Reyna[2]

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Glioblastoma is one of the most aggressive cancers of the brain. Its ability to avoid apoptosis and rapidly invade cells are part of what causes this cancer to be lethal. Our research investigated the role of cannabidiol (CBD) and an AKT 1 / 2 inhibitor. AKT is in a common family of drugs used for their anti-oncogenesis properties. While CBD has recently garnered attention for its potential in cancer treatment, little is still clear. We used cell viability and migration assays (U87-GBM cell lines) to determine the efficacy of each drug. It was found that as concentrations of AKTi increased, U87 cell viability decreased with 10μM being the most effective treatment. Scratch assays showed that both 5μM and 10μM concertation were highly effective in preventing cell migration. However, our results with CBD were much less clear. CBD can be bought through both verified or unverified sources. With this in mind, we modified our experiments to test the efficacy of several sources of CBD compared to known control. Our research was conducted as a class course embedded undergraduate research experience (CURE) using "Cell Block" modules developed by the Cell Biology Education Consortium (CBEC-www.cellbioed.com). Results will be presented.

ASB Lightning Talks

78 - Utilizing a live cell approach to investigate the role of phospho-polyubiquitin in the recruitment and retention of Parkin at the mitochondria

Jiwoo Park, David E. Nelson

Middle Tennessee State University, Murfreesboro, TN

The PINK1:Parkin mitophagy pathway is a quality control process that directs the destruction of damaged, depolarized mitochondria. Mutations within the *PINK1* and *PRKN* genes that encode PTEN-Induced Kinase 1 (PINK1) and Parkin, respectively, are associated with juvenile onset forms of Parkinson's Disease. At polarized mitochondria, PINK1 is imported into the mitochondria, where it is cleaved and subsequently degraded by cytosolic proteasomes. On depolarization, PINK1 accumulates at the outer mitochondrial membrane (OMM), recruiting and activating the cytosolic E3 ubiquitin ligase, Parkin, to conjugate polyubiquitin (pUb) on OMM substrates. These pUb chains are phosphorylated by PINK1, creating phospho-polyubiquitin (ppUb), a unique marker of damaged mitochondria that serves as a platform to recruit additional Parkin. The ppUb chains also engage autophagy receptors, facilitating recruitment of autophagic machinery, leading to the isolation of mitochondria within autophagosomes. However, if mitochondria are repolarized at a sufficiently early stage of this process, PINK1 will rapidly dissociate, aborting the process. We have shown that Parkin dissociates at a slower rate, potentially due to its association with the ppUb chains, which are degraded slowly after repolarization. While mutations in *PRKN* have been shown to affect Parkin E3 ligase activity and its recruitment to depolarized mitochondria, it is currently unclear whether these also affect the release of Parkin from the OMM after repolarization. In this this talk, we will describe how a live cell microscopy approach was used to study the role of ppUb chains in Parkin retention after repolarization. We selected two Parkin mutants with differing E3 ligase activity that are recruited at similar rates to the wild type protein after depolarization and then measured their dissociation rates after repolarization. Specifically, we utilized the hyperactive mutant, W403A, and the E3-ligase deficient mutant, R275W. Our preliminary data indicates that R275W Parkin dissociates more rapidly from the OMM than wildtype Parkin.

79 - Color analysis of petals through computer vision: an expansion of traditional field work

Rachel Perez-Udell, Andrew Udell, Shu-Mei Chang

University of Georgia, Athens, GA

Traditional field surveys can be used to explore patterns of geographic variation that can give insights on how populations have evolved, but are labor intensive, require large amounts of time for decent coverage, and short windows of bloom in some flowering plants can make visiting an entirety of a range in a season an impossibility. We present our methods classifying petal color of common herbaceous species *Geranium maculatum*, through online citizen scientist photographs. We automated the process of downloading and classifying images based on petal color (ranges from light pink to dark purple). We compare this method to our traditional field study's results. Computer aided color analysis greatly increased the range of phenotypic data, while yielding similar results to the field study. We discuss limitations and future improvements.

80 - Exploring the Compounding Effects of Common Pesticides on Freshwater Microbiomes

Gabriel Hooper, Nathan Edmondson, John Hoverson, Mark Fischer, Matthew Becker, Kyle J. Harris

Liberty University, Lynchburg, VA

The prevalent use of pesticides throughout the United States has resulted in unintended negative consequences for non-target organisms. Run-off can move multiple pesticides into environments bringing them into contact with non-target organisms that have variable tolerances to pollution. There are limited studies on how the compounding effects of pollutants impact freshwater microbial assemblages. Previous research conducted by our lab observed that acute treatment of common herbicides on crayfish annelid ectosymbionts resulted in mortality. Therefore, we selected a similar combined treatment to investigate the effect of these environmentally relevant pesticide concentrations on the microbial assemblages of the crayfish and their environment (sediment and water).

This project examines these microbial community assemblages (MCA) before and after a 48-hour exposure to 2000 ppb of herbicides (glyphosate, atrazine, and 2,4-D). DNA was extracted and the 16S gene was amplified using PCR. These samples will be sequenced and then analyzed using the bioinformatics software QIIME2. This project seeks to answer two questions: 1) Will acute exposure to pesticides reduce bacterial diversity and richness within a freshwater environment (water and substrate) and on biota (crayfish)? and 2) Will the exposed MCA reveal that some bacterial populations are more resilient under acute pesticide exposure? We expect that acute pesticide exposure will: 1) reduce bacterial diversity and richness across sample types and 2) that the acute exposure will result in a shift in bacterial populations which predominate in the resulting MCA's. This study seeks to improve our understanding of how an acute exposure to pesticides may restructure microbial communities on crayfish hosts and freshwater environments.

81 - Competitive dynamics among native and invasive aquatic mammals in Arkansas

Rory Carroll

Southern Arkansas University, Magnolia, AR

Native aquatic mammals, especially beavers (*Castor canadensis*), underwent a dramatic population decline in the early 1900s throughout North America. Nutria (*Myocastor coypus*) were introduced to the landscape – intentionally and unintentionally – as a furbearing species

and quickly colonized large areas of the southeastern United States. They were common in Arkansas by the late 1960s and are currently recognized as a nuisance species capable of destabilizing physical and biotic properties within their range. Recent conservation efforts have led to a resurgence in native beaver and muskrat (*Ondatra zibethicus*) populations, and all three of these aquatic mammal species currently occupy most counties in Arkansas. Some evidence suggests that nutria can limit populations of other aquatic mammal species due to overlap in diet and habitat requirements. However, little is known about how these species compete for space and trophic resources or what the population-level impacts of this competition may be. Beginning in 2020, I aim to assess competitive dynamics and niche partitioning between aquatic mammals in southwest Arkansas in three ways. First, I am developing an efficient protocol for using eDNA to assess abundance of aquatic mammals living in lakes. Second, I will use stable isotopes to explore the trophic ecology of each species relative to the presence or absence of competitors. Finally, using cortisol in hair as a proxy for long-term physiological stress, I will examine potential links between conspecific or competitor density, diet, and stress. A greater understanding of the ecology of these sympatric competitors will have major implications for the management of their populations, will inform efforts to mitigate damage from overabundant populations, and has the broad potential to advance competition theory in ecology.

82 - The silk from *Simulium innoxium* larvae: when it should be wettable and when it should not

Tiffany Yeung[1], Bochuan Sun[1], Artis Brasovs[1], Charles Beard[2], Peter Adler[2], Konstantin Kornev[2]

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Black flies are a family of aquatic insects with about 2,300 species in the order Diptera. They can be found throughout a wide range of environments, with each species having an optimum pH and temperature, and some species having an ability to tolerate pollution. The larval stage is mostly spent filter-feeding while attached to solid surfaces, such as rocks and vegetation, in flowing water. The larvae produce silk that is used for many purposes, such as attachment, "life lines", and cocoons for their pupal stage. The silk is produced in their large, paired silk glands. In this study, the contact angle of the silk from *Simulium innoxium* larvae was measured using two methods with three different solvents: distilled water, hexane, and hexadecane. The first method was the drop on fiber method whereby micro droplets were sprayed onto silk strands gathered from the larvae, using forceps, and then analyzed. The second method was the capillary rise method. Larvae were hung from their silk strands and dipped into a cuvette where the silk's meniscus was analyzed. From these experiments, it was found that the silk strand is hydrophobic.

83 - Measuring the initial impacts of the Emerald Ash Borer (*Agrilus planipennis*) in a Green Ash (*Fraxinus pennsylvanica*) dominated Piedmont Swamp Forest in Rowan County, NC.

Matthew Rodriguez, Jay Bolin, Madison Kluge

Catawba College, Salisbury, NC

The Emerald Ash Borer (EAB) is a recent invasive species in the central piedmont of North Carolina. Our goal is to measure the decline and the patterns of change in a Green Ash dominated swamp forest in the Catawba Colleges's Fred Stanback Jr. Ecological Preserve. In fall 2020 we established six, 200 m^2 plots using a nested plot design to measure changes in canopy, sapling-shrubs, and herbaceous vegetation. Our canopy data indicated a relatively low diversity in the tree canopy, trees importance values in descending order (of the top 5), Green Ash (*Fraxinus pennsylvanica*), Sweet Gum (*Liquidambar styraciflua*), Red Maple (*Acer rubrum*), Black Willow (*Salix nigra*), and American Elm (*Ulmus americana*). The canopy was dominated by Green Ash, accounting for 80% of trees greater than 10 cm dbh. Green Ash trees infected with visible signs of EAB had "D" shaped EAB exit holes in the bark, larvae galleries under the bark, and adventitious bark sprouts, accounted for 20% of the total number of Green Ash trees evaluated.

84 - **Detection of the Asian swamp eel (*Monopterus albus*) using environmental DNA**

Samantha Sierra-Martinez[1], Tara Desporte[1], Mark Meade[2], Tammy L. Laberge[1]

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The Asian swamp eel (*Monopteros albus*) is an air breathing, sex reversing invasive aquatic animal that has the ability to disperse over land. This species has no natural enemies and is an opportunistic predator of small aquatic animals, such as fish, crustaceans, and insects. The Asian swamp eel has been observed in South Florida, but little information is available about distribution. The use of environmental DNA (eDNA) is supplementing traditional methods of species detection. Species specific molecular probes have been used in recent years to detect the presence of a species at very low densities. We used eDNA to detect the presence of the Asian Swamp eel in bodies of freshwater in and surrounding North Miami, Florida. A 0.45 micron filter was used to collect water (3-8 Liters) from Amelia Earhart Park, Snake Creek, and Miami Lakes by using the ANDe Smith-Root eDNA sampling backpack. DNA extractions were performed on the filter using the Qiagen Power water kit. The APEX Smith-Root backpack electro fisher was utilized alongside eDNA sampling. Species specific probes were verified using DNA extracted directly from swamp eels which, following PCR, was sequenced by an independent lab (Europhins). We report these findings as well as insight on the presence of other invasive species in the region.

158 - The effect of β-adrenergic drugs on calcium flux and heart rate in Ciona intestinalis

Caitlyn Bernardini, Heather Evans Anderson

Stetson University, Deland, FL

Heart failure and cardiac arrhythmias are characterized by molecular abnormalities involving calcium flux that disrupt the normal functioning of the heart. The effects of β -adrenergic agonists and antagonists on Ca2+ sequestration in the sarcoplasmic reticulum (SR) can result in decreased contractility and altered cardiac function. The purpose of this study was to examine the effects of β-adrenergic drugs on a simple myocardium in the animal model system, Ciona intestinalis. Acebutolol HCl (antagonist) and Isoprenaline HCl (agonist) were

used to dose adult Ciona hearts. Heart beats were examined and quantified in treated versus control hearts. In addition, a fluorescent calcium indicator was tested in an attempt to examine the flow of calcium in the myocardium after drug treatment; however, calcium flux was not observed.

159 - Investigating the Ecological Relationship Between North American Pitcher Plants and Tree Frogs

Tyler Annarino

Marshall University, Huntington, WV

Pitcher plants heavily rely on nectar deposits, scent, and color attractants to entice insects into their traps. Historical records and recent studies show that other insectivores take advantage of these attractants, stationing themselves on carnivorous plants and establishing their hunting grounds on or near the traps. In North America, there are historical records of plants in the carnivorous plant family Sarraceniaceae hosting several predators- both invertebrate and vertebrate alike. In particular, records of green tree frogs (*Hyla cinerea*) hiding within yellow trumpet pitchers (*Sarracenia flava* L.) date back to observations made in the 1800s. Despite continuous observations of *H. cinerea* within *S. flava* pitchers since, the relationship between these two is poorly understood. In this study we will determine if the relationship *H. cinerea* has with *S. flava* is parasitic or mutually beneficial in nature. We hypothesize that, though the frogs are provided with shelter and hunting grounds in which they steal *S. flava* prey, their presence will positively influence growth of the plants by providing nitrogen and phosphorous through urate and fecal deposits. To determine this, we will conduct an ex-situ experiment in which frog presence will be the main variable. We predict that plants exposed to a frog treatment will grow proportionately larger during the trial. Though we expect to see a positive correlation between frog presence and plant growth ex-situ, there is a severe lack of data to support whether *H. cinerea* frequent pitcher plants enough to have a large impact on the plants in the wild. Because of this, we will also conduct in-situ observations of *S. flava* in search of *Hyla* species. While we don't anticipate a high-yield of physical observations of *Hyla sp.* individuals within pitchers, through eDNA sampling we predict that we will find evidence of frequent use of pitchers by *Hyla* species.

160 - Possibility of Earlier Sex Determination of Indigo Buntings by Plumage Differences

Kafayat Oketade, Jill Penn, Maribel Fernandez, Mia Malloy

Georgia Gwinnett College, Lawrenceville, GA

The Indigo Bunting is a migratory bird found in the Eastern half of the U.S. and Mexico. Adult males and females that are breeding are easily identifiable, the males by their bright, deep blues and females by their brownish countenance and sparse blue highlights on the tail. Younger Indigo Buntings can have lesser hints of blue. While some hatch year males have blue feathers prior to their first prebasic molt, it is generally assumed that there are some hatch year males that don't display blue feathers until after their first prebasic molt. Therefore, the absence of blue feathers on hatch year birds is not enough to indicate female, thus sex cannot be determined by plumage alone. To test this hypothesis, feather samples from hatch-year Indigo Buntings were collected and sex was determined by the sex-specific PCR amplification of the CHD-1 gene. Preliminary results suggest that it might be possible to determine the sex of Indigo Buntings by plumage differences at earlier stages than previously documented.

161 - Evaluation of anticancer properties of traditional medicinal herbs using zebrafish tumor xenografts

Brooklyn Wilson, Vinoth Sittaramane

Georgia Southern University, Statesboro, GA

Medicinal herbs have been an interest in anticancer therapies and some have shown properties that can potentially decrease or inhibit the growth of cancerous cells. *Aegle marmelos*, common name vilvam, is found in central and south Asia and is considered a perennial tree. This tree has fruit and leaves that have been used for its medicinal qualities. It has many unique properties that include: anti-inflammatory, antibacterial activity, cold and flu relief, improve metabolism, laxative aid, and can aid in heart and brain disorders. *Anderographis paniculate,* common name periya nangai, is found in dry forests of India. This herb contains glycosides, alkaloids, and flavonoids that can aid in creating antidiabetic drugs. Both herbs have been used for many years to serve many other purposes, therefore we would like to know if they will cease cancerous growth. These herbs were diluted such that early life stages of zebrafish could survive, but cancerous activity could also be inhibited or decreased. Zebrafish have fast life cycles so daily observation is required. These herbs are typically ingested, but in this case, they will be made into a solution, in which zebrafish may live and develop. The dilutions consisted of E3 solution mixed with each herb, and each solution was changed daily. Phenotypes of the fish, mortality, and the pace of developmental cycles were also recorded daily. After the third day of the trial, heart rate was observed to ensure herbal solutions were not detrimental to zebrafish organs, their abilities to swim or float, etc. To assess their anti-cancer potential, zebrafish larvae transplanted with human cancer cells will be treated with optimal concentrations of the herbs and will be analyzed for targeted cancer cell death. These studies will greatly enhance our ability to prevent and treat cancer using traditional medicinal herbs.

162 - A Tiny Lab for Tiny Tardigrades!

C. Brian Odom

Wingate University, Wingate, NC

In most Biology departments space is at a premium and is often a limiting factor when it comes to undertaking new research endeavors. Using readily available furniture and components, I have managed to create a very minimal, but functional Tardigrade lab in only about nine square feet of space.

163 - Duikers, dik-diks, and dwarfing horses... oh my!

Abigail D'Ambrosia

Southern Arkansas University, Magnolia, AR

Current research is showing that many of today's species are shifting their ranges to higher latitudes in response to rising global temperatures and shifting climatic regimes. This presents an interesting problem for species following Bergmann's rule: Larger-bodied organisms at higher latitudes may be replaced by smaller-bodied organisms shifting from lower latitudes. Here, I present data from both the central African blue duiker and Maxwell's duiker (*Philantomba montilcola* and *Philantomba maxwellii*, respectively), as well as the dik-dik (*Madoqua* spp.) in order to determine if they follow Bergmann's rule. *Philantomba* and *Madoqua* are the focus of this study for two reasons: (1) both are an important food source for humans and other predators of central Africa, and may inform us on climate-driven responses of species occupying similar ecological and cultural niches in the US, such as deer. (2) Duikers and dik-diks are ideal analogs to early fossil equids that showed evidence of dwarfing during times of extreme global warming, hence they may help paleobiologists better understand what drove climate-associated decreases in body size. Analyses of tooth size measurements (a proxy for body size) collected from museum specimens show that duikers follow Bergmann's rule with a statistically significant positive correlation between body size and latitude (r^2 = 0.1811, n = 172, p < 0.0001), and dik-diks follow precisely the opposite pattern with a negative correlation between body size and latitude (r^2 = 0.4636, n = 125, p < 0.0001). Future work will attempt to uncover what drives the striking difference in latitudinal-body size patterns between the two seemingly similar species occupying similar niche spaces, as well as attempt to detect any shifts in geographic range and body size in response to present day climate warming.

164 - Exploring new coral reef survey methodology to allow for higher classroom inclusiveness

Quaid Pendleberry, Thomas Jones, Alyssa Jones

Marshall University, Huntington, WV

Since the traditional methods for mapping coral reefs are costly and time consuming, the majority of students interested in marine sciences are excluded. The development of new methods of sampling that reduce both time and resource consumption, however, opens the door for introductory reef biology in the classroom and allows for more citizen science opportunities. In this study, we will explore new, more accessible methodology for the assessment of coral reefs. We demonstrated this on a small portion of reef that was sectioned into three parts: reef flat, reef crest, and forereef. After determining central loci for each section of reef, we then selected points based on a random distance and direction. We arrived at each survey point, placed a meter stick and color plate at the location, and photographed in both white and UV light. We did this for each point on each of the three sections of the reef. We analyzed each image taken to determine structural composition. Corals and other reef structure are identified to lowest possible taxa and using the UV images, percent live coral composition is calculated. The data obtained can be used to measure diversity, composition, and a variety of other metrics. The method of surveying conducted is cost effective and requires little skill and equipment. This allows for entry level participation in the classroom setting, given access is available to coral reefs, or other aquatic habitats.

Beta Beta Beta Oral Presentation Abstracts

BBB 1 - Investigating the Effects of JUUL Pod Extracts on Human Oral Microbiota

Brooke Freeman, Sydney Goertzen

Catawba College, Salisbury, NC

Although JUUL technology was recently released to the public (September 2017), it has gained rapid popularity, often with young adults. Only two years later, several lung-related health issues and deaths have been tied to frequent JUUL use. The purpose of this study is to determine the effects of JUUL pod 'juice' on microbes associated with the human oral mucosa. The direct inhibitory effects of JUUL extract were evaluated using a zone of inhibition analysis on two common mucosal bacterial species, *Corynebacterium xerosis* and *Neisseria subflava*. Such bacterial species are of interest due to their proximity to the mucosal layer and their direct association with a healthy human-microbial environment. Disruption of colonization by these species plays a key role in the development of human-microbial imbalances such as inflammatory bowel disease (IBD). In addition to attractive flavors, JUUL e-liquid is composed of nicotine, glycerol, propylene glycol, and benzoic acid. Nicotine, the compound with the highest potential for microbial inhibition, acts as an immunosuppressant and has been linked to an increased incidence of periodontal disease. To test the effect of JUUL pod extracts on these microbial species, various concentrations of JUUL juice (1%-5%) were applied to lawns of *C. xerosis* or *N. subflava*, in addition to controls (nicotine alone at 5% and solvent) and incubated at 37 °C (human body temperature) for 48-72 hours. Zones of inhibition for each treatment, across 10 replicates of each bacterial species, were analyzed for significant differences via ANOVA with a Tukey's post-hoc analysis. This preliminary study represents the beginning of extensive research on this new technology and its long-term effects on the human oral microbiota.

BBB 2 - Baseline biodiversity of the terrestrial biota in an undisturbed hardwood forest slated for road construction.

Christian Malone, Stephen Tidwell

William Peace University, Raleigh, NC

Shady Acres is a relatively undisturbed patch of old hardwood forest in Wake Forest, North Carolina. A small second order stream extends through the site from an area of moderate slope and levels out in a bottomland. The unnamed tributary runs into Smith Creek, which drains into the Neuse River. A road construction project is planned to transect the property in 2020, therefore we performed an initial census of the area in 2017, and then in 2019 began a detailed, long-term study to document the effects of construction on the terrestrial ecosystem. We concentrated our survey along the creek and on tracks of land extending 30 meters on either side of the stream throughout its reach to determine the biodiversity of amphibian and reptile populations. We performed two transects, established a series of zones, and closely quantified our collection efforts. Amphibian and reptile species diversity and abundance were fairly high. Unfortunately numerous anthropogenic factors have already negatively affected the ecosystem. Numerous running and mountain bike trails have been cleared throughout the property. The removal of ground cover, along with the almost daily human presence, has fragmented the site and reduced organismal movement, especially in the salamander and reptile species. These data should be a nice baseline to determine the effects of road construction on the biodiversity of the site, which we plan to monitor throughout the construction and for at least a year after completion to ascertain the long-term effects on these vertebrate populations.

BBB 3 - Baseline biodiversity of the aquatic biota in an undisturbed hardwood forest slated for road construction.

David Jo, Shannyn Varghese

William Peace University, Raleigh, NC

Shady Acres is a relatively undisturbed patch of old hardwood forest in Wake Forest, North Carolina. A small second order stream extends through the site from an area of moderate slope and levels out in a bottomland. The unnamed tributary runs into Smith Creek, which drains into the Neuse River. In 2020, a road construction project is planned to transect the property, which offered a unique opportunity to study the effects of construction on the stream ecosystem. We performed an initial census in 2017, and then in 2019 began a detailed, long-term study to document the water quality and biodiversity of the stream prior to the start of construction. Future studies will be done during and after construction. Although most of the water chemistry tests were within normal ranges for the Central Piedmont region, the macroinvertebrate diversity was lower than expected. Notable siltation due to residential construction on the border of the property may have already affected the biota. The dominant species were pollution-tolerant species of caddisflies, stoneflies, mayflies and dipterans. The most common large invertebrate species was the variable crayfish, *Cambarus latimanus.* Fish populations were dominated by creek chubs (*Semotilus atromaculatus*) and rosyside dace (*Clinostomus funduloides*). Creek chubs are a highly adaptable species that are tolerant of disturbance, silt and pollution. We expect that this species will endure change from construction fairly well. However, the rosyside dace is a sensitive species that is intolerant of turbidity and silt and only does well in clear, cool water in forested areas. In the future, we expect deforestation and siltation from road construction to greatly affect the macroinvertebrate and fish populations.

BBB 4 - A Comparison of Synthetic and Natural Tick Repellant Products on the American Dog Tick (*Dermacentor variabilis*)

Madison Bodnar

Dalton State College, Dalton, GA

Ticks are a wide spread hematophagous parasite in the family *Ixodidae* that can carry disease and transmit infections to their choice of prey via transmitted pathogens. *Dermacentor variabilis* (American Dog tick) can carry Rocky Mountain Spotted fever and tularemia, bacteria that can severely affect dogs and humans and lead to costly medical or veterinary treatment. In general, ticks are often introduced

into the home by companion animals, like dogs and cats, and the use of repellant agents is a key step in protecting humans and pets from tick-borne illnesses. The objective of this study was to test the repellency of a homeopathic, essential oil-based product (Wondercide), compared to a standard, commercial tick repellant (Flumethrin). A control group trial comparing Wondercide and Flumethrin to no-repellant and head to head comparisons, including positive controls, indicates that the essential oil-based product was more effective at repelling *D. variabilis* than the standard commercial product over a 30-minute observation period.

BBB 5 - Opportunistic Pathogenic Tropical Bacteria *Chromobacterium violaceum* found in North Georgia Appalachians: Identification, Mutation, and Modeling Ecological Dispersion through a Trout Stream

Daniel Bennett

Toccoa Falls College, Toccoa, GA

In November 2018, we found a neon purple bacteria in Toccoa Creek, Georgia and identified it as *Chromobacterium violaceum* via differential microbiology cultures including MacConkey (+;Gram-; Lactose-), catalase (+), blood agar (+hemolytic). Antibiotic resistant to: Erythromycin, Novobiocin, Penicillin, Streptomycin, and Tetracycline, but not Chloramphenicol. Safety testing indicated it was not airborne but waterborne. Sequencing by Williams-Bouyer at Texas A&M revealed 99.9% homology with *C. vaccinii* strain M-B5B-1 and >99.8% with multiple *C. violacens* strains. However, these strains are found in tropical latitudes where they can be opportunistic pathogens in immune compromised patients. Intriguingly, after repeated culture *C. violaceum* stopped expressing purple violaceum pigment. Co-incubation with *E. coli* did not induce expression. An aquaponic system was setup with 1 experimental and 2 control tanks to model our *C. violaceum's* potential dispersion from soil throughout a streamside ecosystem. *C. violaceum* was inoculated into the soil of 3 randomly chosen plants and re-isolated 2 weeks later from the soil of 2/3 plants. Experiments to confirm putative spread of *C. violacens* to plants, water, and fish continue. The spread of a formerly tropical pathogenic antibiotic-resistant bacteria to temperate areas is concerning, especially if it can spread via water.

BBB 6 - Modeling the Effects of Human Disturbance on the Temporal Distributions of Common Wildlife Taxa at Local and Landscape Scales

Hunter Merrill

Lander University, Greenwood, SC

Because human activity is so widespread, it is important to understand how wildlife species alter their behavior in response to different types and intensities of human disturbance. The effects of large, long-term disturbances such as clear cutting have been somewhat well studied, but small episodic disturbances such as hiking are often overlooked. We examined the impacts of such disturbances on mammal activity patterns at the micro scale within five sites in South Carolina using camera traps. In addition, we used GIS to analyze larger, landscape-scale disturbances at 1 km and 3 km distances from our camera trap sites to develop models and identify predictors of increased nocturnality. At the micro scale, open habitats, increased human presence, and proximity to man-made structures and surfaces predicted increased nocturnality. At the 1 km landscape scale, recent changes in land use, more open habitats, and lowered proximity to water predicted increased nocturnality. At the 3 km landscape scale, increased road density, more agricultural land, and higher concentrations of low-level human developments predicted increased nocturnality. In an environment that humans will continue to disturb, understanding how anthropogenic perturbations can affect wildlife behavior at different spatial scales will remain crucial to making informed land management decisions.

BBB 7 - Assessing spread of the invasive Joro Spider in Georgia using population genetics

Hannah Cole

BBB Student, Oakwood, GA

Invasive species are among the leading causes of declines in threatened and endangered native species. The Joro spider (Nephila clavata), native to Asia, is a recently-introduced species in Georgia which has become common throughout northeast Georgia. They were first recognized in 2015 in Colbert, Georgia and have since spread from northeast Georgia to South Carolina and Florida. Their rapid spread may be the result of ballooning, where spiderlings cast a silk strand “parachute” that will be caught by the wind. Ballooning spiderlings can be transported for hundreds of miles before landing. Spiders could also be transported along human transport networks, in or on cargo containers or goods. Our goals are to assess population genetic diversity at the original site of introduction and to differentiate the role of these two spread mechanisms using population genetic techniques. Samples have been collected at Fort Yargo State Park in Winder, Chicopee woods in Oakwood, and at Elachee Nature and Science Center in Gainesville. Our results may suggest that the introduction occurred in a single location followed by natural spread of spiders via ballooning, or may indicate that spiders were introduced in several locations or secondarily transported via the movement of goods. Given their rapid spread and abundant population, the Joro spider is bound to have a strong effect Georgia's ecosystem. Thus, our project has the potential to inform invasion ecology researchers and resource managers and may suggest the need for prompt management action to limit the impact of this newly-arrived predator.

BBB 8 - Antibiotic Resistance in Veterinary and Environmental Strains of *Pseudomonas aeruginosa*

Rashea Smith

Midway University, Midway, KY

Pseudomonas aeruginosa is a ubiquitous gram-negative bacillus shaped bacterium. It is an opportunistic pathogen in human and animal infections that has become very problematic due to its extreme resistance to antibiotics in addition to its ability to rapidly gain resistance to new antibiotics. It is especially concerning for those who are immunocompromised and those who are suffering from other infections. In

this study, twenty-two samples which came from veterinary clinical and environmental sources were examined. Each sample was tested in triplicate against eight classes of antibiotics: penicillins, carbapenems, beta-lactams, fluoroquinolones, cephalosporins, aminoglycosides, macrolides, and broad spectrum. The specific antibiotics included ampicillin, meropenem, aztreonam, ciprofloxacin, ceftazidime, gentamicin, streptomycin, erythromycin, and chloramphenicol. The Kirby-Bauer test results were used to determine whether the sample was resistant, intermediate, or susceptible to each antibiotic. Overall, there were more resistant veterinary samples than environmental samples. This could be due to the fact that *Pseudomonas aeruginosa* strains commonly seen in a clinical setting are likely exposed to a larger number of antibiotics than those found in the environment, therefore are gaining resistance more rapidly.

Beta Beta Beta Poster Presentation Abstracts

BBB P1 - ***Identification of Potential Antibiotics against A. baumaunnii using Virtual Screening Software***

Jordan Ward

Jacksonville University, Jacksonville, FL

Antibiotic resistance is a major obstacle in medicine, and many pathogens can rapidly develop resistance to new antibiotics as they are developed. Acinetobacter baumannii is a gram-negative pathogen that is becoming increasingly problematic in medicine due to its ability to persist in hospital settings and to readily develop multidrug resistance to most antibiotics. One of the ways that it develops antibiotic resistance is by modulating the permeability of porins to reduce the amount of antibiotic that enters the cell, preventing the uptake of an effective dose of antibiotics. Omp-33 is an outer membrane protein that is essential for the cytotoxicity of A. baumaunnii and controls the influx and efflux of water into and out of the cell. By reducing the amount of water and hydrophilic substances that enter the cell, A. baumaunnii can develop resistance to antibiotics. The goal of this project is to use a computer program to screen a library of compounds to identify a molecule that can bind to the RNasE in A. baumannii. We hope that an inability to modulate membrane permeability will allow the influx of clinically relevant levels of antibiotics and reduce or eliminate antibiotic resistance in A. baumannii. We previously used the computer program PyRx to screen a compound library from ZINC15 to identify molecules that bind to the protein target RNasE and selected the molecules with the best binding affinity. The future work is to test the top six compounds, as determined by our previous CADD study, for antimicrobial activity against *A. baumannii.*

BBB P2 - Efficacy testing of NaCl concentrations on *Streptococcus mutans* biofilm production

Arnith Eechampati, Anjali Patel, Gautham Mudireddy

Mercer University Department of Biology, Macon, GA

Antibiotic resistant bacteria are a long-standing result of the improper and over-use of antibiotics. Novel classes of therapeutic antimicrobials are thus, of interest, to the healthcare community. A potential mechanism of preventing virulence is the inhibition of the production of the bacterial extracellular matrix called biofilm. Biofilms allow bacteria to adhere to structures, such as the surface of a tooth, and to avoid the immune system. One bacterium, *Streptococcus mutans*, secretes biofilm which increases its ability to cause dental caries. The ability to produce biofilm results from cell to cell communication through a process called quorum sensing. Quorum sensing occurs when bacteria reach a certain density and signals produced by the bacteria are in a high enough concentration to initiate signal transduction pathways that result in biofilm production. The synthesis of novel lead compounds that mimic the signaling molecules, but do not initiate the signal transduction pathway could effectively inhibit biofilm formation and allow the immune system to impede the host cells of bacteria. Several of our novel lead compounds inhibit biofilm production in *Streptococcus mutans*, but the crystal violet assay needed improvement. Several renditions of testing biofilm production varying overnight culture incubation times and additional NaCl concentrations demonstrated that the addition of 0.25 M NaCl to TSB with 0.25% glucose produced maximal biofilm for testing in the crystal violet assay. Several renditions of testing an additional media and how maximizing biofilm production by altering the media affects the assay of our novel lead compounds will be shared. Production of a greater amount of biofilm should maximize our testing ability of novel lead compounds in the future.

BBB P3 - Enhancing Biofilm Production Assays in Various Media and Salt Concentrations to Build a Novel Competitive Inhibitor Database

Jay Patel, Jeff John

Mercer University, Macon, GA

Quorum sensing is a communication system that is used by single-celled bacteria and fungi to form extracellular matrices called biofilms. The formation of biofilms allows for organisms to have a resistance to anti-microbials. The tolerance which these microorganisms acquire contribute to biofilm-associated infectious diseases. Hence, specific biofilm-inhibiting antimicrobials can add to and strengthen the repertoire of existing pharmaceuticals. We have synthesized and tested over 300 novel lead compounds resembling quorum-sensing signaling molecules and have discovered that 28 of these compounds inhibit biofilm formation in one or more of these species: *Bacillus subtilis, Escherichia coli, Staphylococcus aureus, Streptococcus mutans, and Pseudomonas aeruginosa*. We use a modified crystal violet assay to test inhibition of biofilm production and wish to expand the repertoire of species we can test with our assay. Six additional species (*Enterococcus faecalis, Enterobacter aerogenes, Candida parapsilosis, Candida albicans, Vibrio fischeri,* and *Proteus mirabilis*) that are important in disease have demonstrated maximal biofilm production when media is enhanced with various NaCl concentrations. The preferred conditions are currently being used to test our collection of over 300 novel lead compounds to determine if any of the drugs can specifically inhibit biofilm formation in one of these species. The enhanced database will inform future cohorts information for additional drug design.

BBB P4 - The Effect of Levonorgestrel on Breast Cancer Progression

Victoria Moore, Lindsey Evans, Zemariah Sanders

Mary Baldwin University, Staunton, VA

In the United States, approximately 1 out of 8 women will develop invasive breast cancer over the course of her lifetime. Many of these invasive breast cancers express the estrogen and/or progesterone hormone receptors. Although numerous studies have described the carcinogenic role of estrogen in breast cancer, the role of progesterone has yet to be elucidated. We hypothesized that levonorgestrel, a synthetic progesterone found in birth control, would promote breast cancer progression. To test this hypothesis *in vitro*, progesterone

receptor positive T47D breast cancer cells were treated with 0.1 nM levonorgestrel for 72 hours. Cellular viability assays demonstrated a significant increase in proliferation and no change in cellular death. Real-Time RT-PCR revealed significant changes in epithelial-to-mesenchymal-associated genes, E-cadherin and TWIST. Currently, *in vivo* applications of the effects of levonorgestrel on breast cancer are being done in zebrafish. The zebrafish embryos are microinjected with T47D cells and upon incubation with levonorgestrel the zebrafish are analyzed for cell proliferation and metastasis at 4 dpi. We are currently developing a more cost effective method to visualize the cancer progression that does not use a fluorescent labeling, but offers a way to visualize the metastasis of xenotransplanted human T47D breast cancer cells through the use of immunochemical staining of whole mount embryos and light microscopy. The embryos are being preserved and whole mount immunochemically stained using anti-human KU80 antibody, detecting a protein found in DNA. The KU80 antibody is specific to human cells and allows for differentially staining of the cancer cells without cross reacting with zebrafish cells. Once the fish have been stained they are paraffin-embedded, sectioned (5 μM), and analyzed for cancer progression using light microscopy. Future studies will continue to investigate the effects of levonorgestrel on breast cancer progression, using both an *in-vitro* and *in-vivo* model.

BBB P5 - Possibility of ROBO1 Binding with Ankyrin as a Mechanism for SLIT1-Regulated Axon Guidance

Maryellen Haas

Marymount University, Arlington, VA

The formation of neural circuitry without neurodevelopmental or neurodegenerative disorder rests upon precise axonal guidance (Stoekli, 2018). The established signalling between the axonal growth-cone receptor Roundabout homolog 1 (ROBO1) and the chemorepulsant, SLIT, facilitates midline crossing to maintain course towards the cellular target (Alavi et al., 2016). This signalling mediates axonal turning through actin polymerization or disintegration within the growth-cone, though the protein players of this mechanism remain unestablished. Studies (Levinger & Wright 2017; Schlatter et al. 2007) revealed binding of close-homolog of L1 (CHL1), a colocalized partner of ROBO1, with the scaffolding protein Ankyrin to establish spectrin linkages with actin filaments for axonal elongation or collapse. Extending this mechanism, we explored the possibility of ROBO1 and Ankyrin colocalization, which would suggest a possible role in the SLIT-mediated repulsion mechanism. Repeated trials of indirect immunofluorescence staining of sectioned mouse brains with monoclonal ROBO-1 and Ankyrin antibodies remain inconclusive; however we continue our efforts to establish evidence of a ROBO1-Ankyrin interaction. Understanding the interactions of ROBO1 and Ankyrin provides insight into mechanism of axonal guidance, with applications for studying the causes of neurodegenerative and neurodevelopmental diseases.

BBB P6 - Second-generation κ-opioid agonist as a peripherally-restricted analgesic

Elizabeth Schneider

Erskine College, Due West, SC

Today, μ-opioids are prescribed for peripheral pain, but they come with the risk of many toxicities including gastrointestinal issues, sedation, and addiction. The compound of study, referred to as JT09, has shown peripheral pain alleviation with high selectivity of κ-opioid receptors compared to μ- and δ-opioid receptors; this prevents the drug from having any effect on the central nervous system as it cannot cross the blood brain barrier. JT09 has been incorporated into ProNeura rods, subdural implants that continually administers the drug for up to 12 months. This technology may render the need for oral and intravenous administration unnecessary, as well as decrease the number of addictive drugs available to the public. Rats were implanted with the ProNeura rods and blood samples were taken at various time intervals. Results are expected to show effectiveness of JT09 as a peripheral pain reliever in the ProNeura platform and not cause symptoms like other medications that cross the blood-brain barrier. Future directions include pharmacokinetics studies, as well as immunohistochemistry studies to observe the location, action, and relation of κ-opioid receptors (KORs) with myocardial infarction (MI) size and its influence on other antigens.

BBB P7 - Genetic Analysis of Biofilm Production Pathways in *Streptococcus mutans* Inhibited by Novel Lead Compounds.

Vy Nguyen, Gabriella Longway

Biology Department, Mercer University, Macon, GA

Bacterial virulence is associated with biofilm formation. Biofilms are extracellular matrices that protect bacteria from the host immune system. The formation of biofilm is a cellular response initiated by quorum sensing, the communication system utilized by bacteria. We are interested in understanding the genetic pathways that control biofilm production and have synthesized and tested several biofilm inhibiting drugs that can help us deduce these pathways. We have previously disrupted the process of biofilm formation with novel lead compounds that resemble autoinducers, the chemical signaling molecules used in quorum sensing, that potentially act as competitive inhibitors.

Genetic screens on modified Congo Red plates were used to isolate strains that produce less biofilm than wild type *Streptococcus mutans*. The isolates' diminished biofilm formation are then confirmed with a crystal violet assay, and doubling-times are measured to ensure that a change in growth rate is not the source of a reduction in biofilm. We have isolated several mutants in *Streptococcus mutans* that display decreased biofilm formation and no longer respond to biofilm inhibiting compounds alanine 4-Chloro-3-nitrobenzoic acid and valine 2-Fluoro-5-nitrobenzoic. The mutated pathway is therefore the same pathway acted on by these previously successful compounds. Analyses of the genomic sequences from the isolates will allow us to identify the genes involved in these specific biofilm producing pathways.

BBB P8 - The effects of BPA and BPA derivatives on *Daphnia pulex*

Claire Featherstone, Erin Howard

Catawba College, Salisbury, NC

Bisphenol A (BPA) is an industrial chemical used in the formation of polycarbonate plastics and epoxy resins, which is often associated in the manufacturing of food packaging and water bottles. BPA has been shown to mimic the hormone estrogen, allowing it to react with estrogen receptors and thus affect their function. Previous research has shown that BPA can seep into food or beverages that are contained in BPA packaging, exposing individuals to BPA, which has been shown to increase the risk of adverse health effects on the brain, prostate gland, mammary glands, behavior, and reproduction in lab studies. Thus, BPA was banned from the manufacturing of everyday plastics, like water bottles. BPA has been replaced with BPA derivatives, like BPAF and BPS, which are thought to be more stable than BPA. However, these BPA replacements may have more potent consequences on human health. This research project aims to investigate the effects of BPA and BPA derivative toxicity on *Daphnia pulex*. *D. pulex* are freshwater crustaceans, commonly known as the water flea, that are often used in research as they are easy to reproduce and are sensitive to toxins. Importantly, previous studies have not examined the toxicological and reproductive effects of BPA and BPA derivatives in *D. pulex*. As such, we plan to test BPA, BPAF, and BPS in various concentrations on *D. pulex* survival and immobilization (toxicity). Results from this project will demonstrate the possible effects of BPA and BPA derivative pollution on *D. pulex*, which may have significant consequences on freshwater ecosystems.

BBB P9 - Subspecies status of a disjunct population of the Black-throated Green Warbler (*Setophaga virens*)

Macayla Upright

Catawba College, Salisbury, NC

The Black-throated Green Warbler (*Setophaga virens*) has two allopatric subspecies in North Carolina: *S. v. virens* breeds in the Appalachian Mountains, and *S. v. waynei* breeds in the Coastal Plain. In recent years, *S.v. virens* has increased in abundance whereas *S.v. waynei* has declined and is now on the North Carolina list of state endangered species. There is a disjunct population of *S. virens* that breeds in the Uwharrie Mountains of central North Carolina that has been there for decades but is little studied. Our project aims to discern if this population is *S. v. virens* or *S. v. waynei*. To determine genetic similarities between these three populations, we modified a molecular assay targeting the cytochrome oxidase 1 (CO1) gene (Emura et al., 2013) from blood and tissue samples. After successful adaptation of the methods in our lab, we have processed and sequenced samples from the field. This project has the potential to identify a new population of the North Carolina state-endangered *S. v. waynei* subspecies.

BBB P10 - Phylogenetic Placement of an Unidentified Crayfish Species in Southwest Virginia

Samuel Barnette

Emory & Henry College, Emory, VA

A population of unidentified blue crayfish was discovered at the Emory & Henry College- Bartlett-Crow Field Station. The hypothesis being tested is whether this is a new species, or if it is a sub-population of a suspected relative, such as *Cambarus monongolensis*. We have observed thus far that the unidentified species creates burrows above ground in a wet former flood plain meadow previously used for cattle but is now being reclaimed as wetland. For comparison, we are using 16S and 28S mitochondrial genes for sanger sequencing, followed by comparing phenotypic expressions to proposed relatives. The findings of this study will provide the basis for future research on the putative taxon nova.

BBB P11 - Effects of heavy metals in soil water content on electrical signals in plants

Kayla Heinz

Dalton State College, Dalton, GA

Plant signaling (plant neurobiology) is a field of plant biology research that aims to understand how plants respond to the external environmental stresses by generating electrical signals at the roots to the stems and leaves or vice versa.

Hyperaccumulators are plants capable to tolerate, absorb, extract, and accumulate large amounts of metal compounds in their organs compared to non-hyperaccumulator plants. They are very efficient in phytoremediation processes for cleaning up contaminated soil and water from organic and heavy metals contaminants.

This study is aimed to measure the integrated signaling (electrical potential, EP) in hyperaccumulating plants (roots, stems, and leaves) to grow and reproduce optimally in contaminated environment by heavy metals. We will study how plants generate and transmit these signals in response to the soil water content. In addition, we will study the physiological responses of plants associated with the electrical potentials of plant tissues.

Mature plants, in five replicates, will grow in a compost soil in 7 L plastic containers. Plants will be irrigated with 4L of water once per day in morning. Electrical potentials will be measured at 1 min intervals once the plants are treated with different levels of mercury and arsenic. Plants will be grounded from the environment by a “Faraday cage” to prevent external electromagnetic signals in the greenhouse from interfering with electrical measurements.

The electrical potential will be measured using microelectrodes as described by Gil et al. (2009), Gurovich and Hermosilla (2009), Oyarce and Gurovich (2010) and Sawyer et al. (1995). Microelectrodes will be inserted into the stems and leaves while a reference electrode will be inserted into the potting medium at the base of the stem. Electrical potential differences between each set of electrodes will be

determined from EP measurements.

BBB P12 - The Prevalence of Antibiotic Resistance in the Gut Flora (Enterobacteriaceae) of Wild Horses in Carova, NC and Grayson Highlands, VA

Madison McKinsey

Emory & Henry College, Emory, VA

A horse's gastrointestinal tract houses a large and diverse microbial community. Antibiotics used for prophylaxis and/or treatment of bacterial infections can lead to the evolution of antibiotic resistance in the horse's gut flora. For this study, fecal samples of wild horses from the Outer Banks, Carova Beach, NC and wild ponies from Grayson Highlands, VA were analyzed to determine the prevalence of antibiotic resistance against twelve common antibiotics used in the veterinary treatment of domesticated livestock. We expect the flora of wild horses to be more susceptible to these antibiotics than domesticated horses due to a lower frequency of medical intervention as compared to domesticated horses. We plan to compare the degree of resistance of the wild population to the Emory & Henry Equestrian Center horses.

The Carova Beach population was 100% resistant to Bacitracin, Clindamycin, and Penicillin, 4.35% resistant to Ampicillin, 86.96% to Chloramphenicol, and 8.69% to Erythromycin. The population was 100% susceptible to Ciprofloxacin, Doxycycline, Gentamycin, and Tetracycline, and 95.65% susceptible to Vancomycin. The Grayson Highlands population was 100% resistant to Amoxicillin, Ampicillin, Bacitracin, Clindamycin, Vancomycin, Erythromycin, Penicillin, and Tetracycline. The population was roughly 60% resistant to Chloramphenicol, Gentamycin, and Doxycycline. The only antibiotic with levels of susceptibility was Ciprofloxacin at 32%.

These data suggest a moderate degree of exposure of the Carova Beach herd to either antibiotics, or bacteria exhibiting resistance to some of these antibiotics and a higher degree of exposure in the Grayson Highlands. One possible hypothesis is exposure to drinking water pools contaminated with human feces from septic systems that are periodically inundated during high rain periods in the area of the Outer Banks and the tight knit population and access to medical intervention in the area of the Grayson Highlands.

BBB P13 - Systemic Inflammation in a Transaortic Constriction Model of Heart Failure

Morgan Callaghan

Emory & Henry College, Emory, VA

Heart failure is one of the main causes of death globally yet there is no cure. Vagus nerve stimulation has been shown to have the potential to be a better treatment for heart disease. The purpose of this study was to determine differences in the amount of inflammation present in rats that have been induced to heart failure. Heart failure was caused by tying the aorta between the brachiocephalic artery and the left common carotid artery. The amount of inflammation was found by determining the abundance of inflammatory proteins TNF-alpha, IL-1, and IL-6 through use of ELISA assays. Each of the assays was read using a spectrophotometer at 450 nm. Analysis of these results was done by graphing the standard curve and using the equation to determine the concentrations of inflammatory cytokines in each sample. It was determined that none of the samples had any significant concentration of any of the inflammatory proteins. This leads to the belief that rats are not a good model for systemic inflammation in heart failure.

BBB P14 - Flow cytometry reveals a cryptic *Isoetes* complex at Broxton Rocks Georgia

Kory Ly[1], Nathaniel Robbins[1], Frankie Snow[2], Peter Schafran[3], Jay Bolin[1]

[1]Catawba College, Salisbury, NC, [2]South Georgia State College, Douglas, GA, [3]Boyce Thompson Institute, Ithaca, NY

Polyploidy and reticulate evolution are important drivers of speciation in *Isoetes*. We present preliminary data on a cryptic *Isoetes* complex that occur in shallow pools on Altamaha Grit sandstone outcrops in the coastal plain of Georgia. Several lines of evidence including direct chromosome counts, flow cytometry based genome size estimates (of over 70 individual plants on eight different outcrops), and morphology, reveal three putative new taxa: a diploid, tetraploid, and sterile triploid plants. The triploid plants were the least frequent, had intermediate C-values, and displayed misshapen megaspores suggesting sterility. Moreover, we will discuss ongoing DNA based lineage sorting work to assist in definitions of species boundaries.

BBB P15 - Investigation of the toxicological effects of CNT-Ab in mice following microwave hyperthermia two weeks post-treatment

Andrew Mixson

Georgia Southern University, Statesboro, GA

Serious side effects and treatment resistance are the main impediments to successful cancer therapy. A variety of nanoparticles have been used for localized, site-specific treatment that prevent or circumvent these impediments. Microwaves alone have been previously used for thermal ablation of various tumors, setting precedence for their successful use in live organisms. In cell culture studies, it has been observed that multiwall carbon nanotubes (MWCNTs) instantly and efficiently absorb microwaves, causing hyperthermia of cells in direct contact with them with unnoticed harm to other cells. It is hypothesized that a treatment can be developed based on a safe microwave heating schedule for the selective ablation of tumor cells *in vivo* using MWCNT-ab conjugates as a targeting medium and mice as animal models. This will be accomplished by conjugating MWCNTs with anti-PSMA antibodies (ab) in order to induce the selective uptake of MWCNTs by PC3 cells, known to significantly over-express PSMA antigens in comparison to non-cancerous cells. This study seeks to elucidate any toxicological effects by the characterization of MWCNT-ab distribution, clearance, and toxicology in mice following

microwave hyperthermia.This will be assessed through clinical chemistry and analyzing gene expression in the brain, liver, and kidney.

BBB P16 - An update to genome size estimates for eastern North American *Isoetes*

Nathaniel Robbins[1], Peter Schafran[2], Kory Ly[1]

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The genus *Isoetes* is well known for morphological convergence and a lack of reliable characters for field identification. Polyploidy and reticulate evolution are important drivers of *Isoetes* diversity. Thus, the chromosome complements of *Isoetes* spp. are key attributes for species delimitation. By using a rapid DNA flow cytometry protocol, we generated several hundred novel C-values, a measure of DNA quantity, for diploid, tetraploid, hexaploid, and one octoploid *Isoetes* species from North America and Europe. As expected we observed a significant positive correlation between C value and chromosome complement, though C-value alone in many cases is also not a reliable predictor of ploidy. Several examples of sterile hybrids in *Isoetes* display near perfect C-value intermediacy relative to their putative progenitors.

BBB P17 - Determining effects of road construction on stress-related gene expression in fish.

Dalena Nguyen

William Peace University, Raleigh, NC

The purpose of this study is to investigate the physiological stress responses of fish before, during, and after a road construction project over the Wake Forest Creek stream in the town of Wake Forest, NC. Man-made structures such as roads can cause waterways to change in sediment composition, water turbidity, and flow direction. They can also have effects on local wildlife species as their habitats are altered, often permanently. We chose two fish species as our model species; the rosyside dace (*Clinostomus funduloides*) is sensitive to these changes whereas the bluegill (*Lepomis macrochirus*) is not. Although some of the fish will die, we want to know if the stress responsive genes in the surviving fish are helping them adapt to the changes in their habitat. Stress activates the glucocorticoid signaling pathway which has been studied in a variety of fish and mammalian species. Cortisol is the main glucocorticoid hormone in this pathway, and it affects many processes including metabolism, inflammation, and blood pressure. We wish to evaluate levels of cortisol responsive genes at different stages of this construction project to help determine if changes in gene expression in stress responsive pathways change and possibly contribute to the survival of fish during the disruption of their normal habitat. We are focusing on the expression of the Akt, protein kinase A, and protein kinase C genes because they are activated downstream of cortisol. The molecular techniques that are involved in this study include RNA/DNA purification, polymerase chain reaction (PCR), reverse transcription-PCR, and western blotting. We hypothesize that there will be an increase in stress responsive genes for both fish species as the road construction progresses, demonstrating a link between human activity and physiological changes in affected wildlife.

BBB P18 - Effects of Heavy Metals (Copper and Lead) on Antioxidant Enzyme Production and Root and Shoot Growth of Two Plants: *Nasturtium officinale* (Watercress) and *Alternanthera philoxerides* (Alligator Weed)

Ginger Bailey, Hannah King

Abraham Baldwin Agricultural College, Tifton, GA

This study examines the effects of copper and lead on *Alternanthera philoxerides* and *Nasturtium officinale,* two wetland-dwelling plants capable of accumulating heavy metals within their tissues. *A. philoxerides*, commonly known as Alligator Weed, is an invasive species native to South America that has been able to thrive here in the U.S. due to its natural defenses in toxic conditions. *N. officinale,* or watercress, is an edible, aquatic herb native to Europe, but its ability to bioaccumulate heavy metals raises concern for those who include this plant within their diet. While both plants are naturally equipped to take up heavy metals from within their environments, *N. officinale* has shown to be more easily stressed than *A. philoxerides*. Heavy metals stress plants by causing them to produce antioxidant enzymes to combat the oxidant enzymes produced from the presence of heavy metals in the plant. The greater a presence of antioxidant enzymes can be correlated to a greater amount of stress to the plant. This can be found by measuring the amount of peroxidases, a type of antioxidant enzymes, and collecting morphometric measurements of the roots and shoots of both plants. Peroxidases were measured by crushing plants introduced to various levels of copper and lead and collecting the luminescence values of each using a benchtop luminometer. Morphometric results were gathered by measuring the length of roots and shoots of the plants after they had been introduced to copper and lead. This study found that though *N. officinale* was stressed by lead, *A. philoxerides* was not stressed by either of the heavy metals, suggesting its tolerance of a range of heavy metals.

BBB P19 - Variation Across the Reproductive Systems of female Sceloporus woodi; Comparing populations from the Long Leaf Pine and Florida Scrub Habitats of the Ocala National Forest

Meghan Turner

Georgia Southern University, Statesboro, GA

The Ocala National Forest is composed of two different habitats: longleaf pine and Florida scrub. Egg size and quantity in gravid *Sceloporus woodi* were compared to each lizard's respective tail-vent length and mass. It was hypothesized that larger females would have larger eggs. Female *Sceleperous woodi* specimens were collected and data was collected from each one. After identifying the eggs present in the scans, the eggs in each gravid female must be counted and measured using image processing software. Egg production will be represented by the total area of egg matter in each lizard. The expected results are a positive correlation between lizard mass and egg production.

BBB P20 - Fungal DNA barcoding and a preliminary checklist of mushrooms at the Fred Stanback Jr. Ecological Preserve in the piedmont of North Carolina

E. Malachi Gray

Catawba College, Salisbury, NC

The purpose of this study is to Identify and catalog the fungal taxa in the Fred Stanback Jr. Ecological Preserve (FSJEP) in the central piedmont of North Carolina. North Carolina Natural Heritage Program has designated portions of the FSJEP as a significant Natural Heritage Area. The FSJEP is approximately 68 ha and is composed primarily of a green ash dominated flood plain and mixed mesophytic hardwood forest. Inventories of most taxonomic groups have been completed with the exception of fungi. To document fungal diversity, specimens were photographed, spore prints made, and samples were collected and accessioned into the Catawba College Herbarium (CATU). Identifications were made morphologically. Taxa within fungal species complexes were barcoded using molecular techniques. We used standard fungal barcoding loci (e.g. ITS) and standard DNA extraction kits. This fungal biodiversity study was initiated Jan 2020 and will continue until at least 2021.

BBB P21 - Removal of Heavy Metals from Polluted Water

Caleigh Eberhardt

Abraham Baldwin Agricultural College, Tifton, GA

Heavy metal pollution has become an increasing problem around the world due to industrialization. Humans are migrating into cities where more factories are being built to compensate for the demands of the increasing population. Factories use and produce heavy metals, which are not biodegradable and therefore pollute local water supplies when disposed of. Heavy metals such as mercury, cadmium, lead, and cobalt are known to be very toxic or carcinogenic to humans. To reduce the high levels of heavy metals in polluted water, we are designing a filter made from Graphene Oxide (GO) and Diatomaceous Earth (DE) Silica. GO was synthesized through the oxidation of Graphene nanoplatelets. The single layer, hexagonal structure, with different polar functional groups, gives it a large surface area making it a very efficient adsorbent. GO that had been purchased was exfoliated to expand the sheets of carbon. Attaching DE Silica makes GO more efficient because the Silica has a uniform, microscopic porous structure that can bind more heavy metal ions. In our preliminary research, we tested the adsorption of the cadmium ion over time on activated Carbon and Silica, separately. We found that adsorption of Cd^{2+} on Carbon was independent of time on the scale we used (1 to 60 minutes), while adsorption of Cd^{2+} on DE Silica was dependent of time with maximum adsorption at 60 minutes. Carbon was a better adsorbent as compared to DE Silica based on the solutions we used (1000ppm and 2000ppm). Our next steps are to synthesize GO attached to DE Silica and determine the adsorption of different heavy metals by the hybrid adsorbent.

BBB P22 - **How High is College Students' Sodium Intake?**

Scott Ventrello

Toccoa Falls College, Toccoa, GA

According to FDA the average American eats 3400mg of sodium per day. The recommended amount is 1500-2400mg per day. [1] How much sodium does a student at Toccoa Falls College consume each day if they eat the cafeteria meal plan? An overabundance of sodium can cause water retention, resulting in edema and hypertension. If excess sodium consumption is coupled with insufficient water intake students will be dehydrated. Another side effect of excess sodium is the calcium deficiency. Excess salt intake increases thirst and thus water consumption, increasing urine, resulting in calcium loss [2].

I tested cafeteria samples' sodium content. Samples were blended in distilled water to dissolve the salt, solids filtered out, and sodium concentration titrated. The indicator was potassium chromate: $AgNO_3$ + NaCl --> AgCl + $NaNO_3$. Students eating a recommended serving from the TFC cafeteria would have consumed 1440mg sodium that day; however, if they had biscuits and gravy, they would have consumed 2391 mg. This is very close to the maximum amount of sodium recommended, but does this represent the average person? From observation, students, including myself, usually eat more than recommended, which means actual intake of sodium would be higher than 2391mg.

[1] "Sodium." *Accessdata.fda.gov*, Food and Drug Association, www.accessdata.fda.gov/scripts/InteractiveNutritionFactsLabel/sodium.html.

[2] Ossola, Alexandra. "Here's What Happens To Your Body If You Eat Too Much Salt." *Popular Science*. N.p., 3 Dec. 2015.

BBB P23 - The Effects of Copper Transfer Between a Metal-Tolerant Host, *Alternanthera philoxeroides*, and a Hemiparasite, *Castilleja coccinea*

Abby Unger

Abraham Baldwin Agricultural College, Tifton, GA

This research will investigate into metal transfer from metal-tolerant hosts to hemi-parasitic plants and the roles and effects associated with these plants. Interactions between the host, *Alternanthera philoxeroides*, and the hemi-parasite, *Castilleja coccinea*, specifically, will be investigated. Hemi-parasitic species maintain the ability to photosynthesize; however, the species is able to grow haustoria, which allows for the transfer of water, nutrients, genes, and numerous types of ions. In metal-tolerant species, accumulation of metals can provide

defense against herbivores, can be potentially toxic in high concentrations, and can also decrease fitness when metals are deficient. This study aims to examine the effects that the transfer of copper ions from host to hemi-parasite will have on the response of the parasite and the host-to-parasite interaction.

BBB P24 - Fish as Environmental Indicators of Fecal Coliform Contamination.

Benjamin Gallimore

Emory and Henry College, Emory, VA

"Fish as Environmental Indicators of Fecal Coliform Contamination"

The epithelial mucosal membranes of *Lepomis macrochirus* (Bluegill) and *Micropterus salmoides* (Largemouth Bass) were swab sampled for the presence of fecal coliform bacteria. Fish from habitats shared with *Bos taurus* (Domesticated Cattle) as well as fish from cattle-exclusion habitats were sampled and compared. Swabbing for fecal coliform bacteria could help indicate water contamination which could prevent the spread of waterborne pathogens. We hypothesized that fish inhabiting water systems that domesticated cattle have access to would demonstrate a higher prevalence of fecal coliform bacteria in their skin mucosa than fish in cattle exclusion water systems. Two ponds that cattle had access to, and two ponds that had no cattle access were sampled. Seventy-eight percent of the fish sampled from the two cattle access ponds (N= 9) showed at least one species of fecal coliform bacteria on their epithelial mucosa, compared to eighty-one percent (N=21) of fish sampled from cattle exclusion habitats. Water samples were taken from each water system to confirm the presence of at least twenty colonies of fecal coliform bacteria per ten microliters. Eighty-five percent of Bluegill sampled (N=7) and eighty-three percent of Largemouth Bass (N=24) had at least one species of fecal coliform bacteria present in their epithelial mucosa, indicating no significant difference among species. Data supported no correlation of increased fecal coliforms in cattle access ponds compared to cattle exclusion ponds. Qualitative data on the habitats indicated that ponds with cattle access were more degraded than those of cattle exclusion, which may account for reduced diversity among species and relative abundance of species in cattle access ponds.

BBB P25 - Environmental Mercury In Domestic Cats

Dina Reyes

Catawba College, Salisbury, NC

Mercury is a highly toxic element that is released into the atmosphere from human activity such as the burning of fossil fuels. From the atmosphere, the mercury settles on terrestrial and aquatic ecosystems and is incorporated by plants and animals. The purpose of this research project is to determine if domestic cats are exposed to environmental mercury by eating foods that contain mercury, or by eating wild birds or mammals that have mercury within their bodies. I have analyzed mercury content in fur samples provided by cat owners. The cat owners complete a questionnaire about the diet and housing of their cat(s). We measure the mercury content of cat fur and cat food with a Milestone DMA-80. The data collection and analysis currently are underway. I will present the latest finding from my project. My research could help cat owners reduce their cat's exposure to mercury by revealing which aspects of cat's diet and housing are correlated with mercury load.

BBB P26 - The Study of Sepallata Genes in Budding Moth Orchids

Riley Piek

I am Riley Piek, Marion, VA

The development of flowers from buds is a process that uses a multitude of different genes. These genes, known as MADS-box genes, have been well described in the ABCDE model. Each letter represents a category of genes responsible for the development of a specific part of the flower. The E category of genes are more unique than the other categories, in the sense that these genes are needed for some of the other category genes to function, such as the B and C genes (Pelaz et. al. 2000). *SEPALLATA* genes are the only known E genes (Huang 2015). There are four variants of the *SEPALLATA* genes, *SEP1*, *SEP2*, *SEP3*, and in *Phalaenopsis equestris* (Pan et. al. 2014). Pan et al. (2014) have studied expression of *SEP* genes in adult *Phalaenopsis equestris*; however, their expression in buds is less understood. Only *SEP3* genes have been investigated further by previous researchers (Dean 2017). Due to the commercial usage of *Phalaenopsis equestris*, and the agricultural and evolutionary knowledge that could be found, this project will use qPCR to investigate the expression pattern of *SEP2* genes.

BBB P27 - The Effects of Probiotic Yeast on the Rumen

Alexandra Barbee

Student, Emory, VA

Bloat in the foregut within ruminant species is common, particularly in those who are considered domesticated livestock. The increase in gas production due to consuming forage that is too rich to be broken down, causes discomfort and even medical complications in the digestive system of the animal. The proper methods on how to treat the symptoms of bloat, these being the use of medications or methods such as tubing the animal to release pressure, are beneficial. However, there is a lack in knowledge on preliminary measures that could be given in order to reduce the chances of bloat. This leads us to ask the question, can the rumen microbiota of goats be manipulated through probiotics such as yeast to prevent ruminal tympany? By testing the use of probiotic yeast in an in vitro, small rumen model, we can observe the levels of gas production as well as pH changes of ruminal fluid used for testing in order to confirm that the use of probiotic yeast would improve ruminal health, and ultimately reduce or eliminate the risks of ruminal tympany. If successful, this could be beneficial to livestock owners, as it would require less energy input in care for the animals, as well as less money required, as treatment

for bloat can be costly.

BBB P28 - Investigating the Differential Absorption of Miconazole in Yeast Cells Incubated with Various Nanoparticle Solutions

Yeimi Reyna Romero

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The benefits of nanoparticles in medicine have allowed an increase of nanotechnology studies in the past decade. These substances facilitate cellular uptake of drugs, and allow for efficient drug delivery in cells. They can also lower toxicity, lessen drug side effects, increase solubility increase biodistribution and overall increase drug bioavailability. In cancer research, nanoparticles are being used to deliver accurate dosages of drug to tumor/cancerous cells without disturbing the function of normal cells. Various types of nanoparticles are used based not only on their biophysical/chemical properties, but the physicochemical properties of the drug being delivered. The effect of metallic nanoparticles such as gold and zinc oxide on drug uptake in eukaryotic organisms has not been studied in depth. Yeast cells serve as a model organism for studying several biological mechanisms, such as the uptake of antifungals, or the effects of specific nanoparticles on viability. Given that nanoparticles may enhance drug delivery in this system, we hypothesized that uptake of the antifungal miconazole in yeast cells would be enhanced by incubation with gold and zinc oxide nanoparticles. The overall findings of this study demonstrate the use of gold nanoparticles along with miconazole, on yeast cells, yielded a significant decrease in cell viability compared to zinc oxide-miconazole or miconazole alone.

BBB P29 - Delimiting cryptic species of the *Anopheles crucians* complex

Nicole Hall

Catawba College, Salisbury, NC

There are seven species associated with the *Anopheles crucians* cryptic mosquito complex: *An. bradleyi, An. georgianus,* and *An. crucians* A, B, C, D, and E. Identification of distinct species is essential as female Anopheles are vectors for several pathogens that cause disease in humans, including West Nile, Eastern Equine Encephalitis, and Malaria. Further, vector efficiency is known to be a primary driver of infectious disease spread in human populations, and even very closely related species may differ in critical aspects such as habitat preference or life cycle development. Morphological identification is made difficult by environmental factors that may alter appearance, such as temperature and sun exposure. In 2004, Wilkerson *et al*. developed a molecular assay targeting the ITS2 gene to help identify members of this cryptic complex. In this study we revisit the ITS2 gene as a potential tool to help differentiate these species at the molecular level, and further begin to unravel the mysteries surrounding distinctive morphological characters within this *Anopheles* complex.

BBB P30 - Investigating the Antimicrobial Properties of Local versus Non-Local Honey on Human Oral Microbiota

Jasmine Wiitala

Catawba College, Salisbury, NC

With the steady rise of antibiotic resistance in microbial pathogens there is an increased demand for new antimicrobial chemotherapies. Several studies indicate that honey varieties inhibit bacterial growth, and this inhibition may be due to specific compounds found differentially in geographically distinct varieties. As honey varies in its chemical composition based on location and plant-associated sources, we questioned whether a raw honey variety from a local producer would possess compounds that would have a greater inhibitory effect on bacteria that were also locally derived. We hypothesized that honey derived from a local source would inhibit bacterial growth derived from a local human population to a greater extent than honey from a geographically foreign region. To test this, two varieties of raw honey obtained from a local producer in Salisbury, North Carolina and a foreign producer from Israel were analyzed using a zone of inhibition assay on randomized saliva samples from students attending Catawba College. The comparative inhibitory properties of local vs. non-local honey metabolites on locally-sourced oral microbiota will be discussed with an emphasis on the different compounds found in each variety that may contribute to limiting bacterial growth.

BBB P31 - Structure and function of the yeast DEAD-box protein Dbp6

Sarah Emerick

Eckerd College, St. Petersburg, FL

RNA helicases are enzymes found across all life forms and are involved in all aspects of RNA metabolism. DEAD-box proteins, the largest family of RNA helicases, are classically defined as RNA-dependent ATPases that unwind RNA duplexes. However, not all DEAD-box proteins have been investigated enzymatically and while many that have do demonstrate RNA unwinding activity, some do not. Elucidating the molecular mechanism of each DEAD-box protein is therefore of interest, especially since many have been implicated in cancer. Here, we are investigating Dbp6, an essential DEAD-box protein in *Saccharomyces cerevisiae* that is required for maturation of the 60S ribosomal subunit. By solving its crystal structure and characterizing its *in vitro* activities, we aim to provide insight into its molecular mechanism. In collaboration with Dr. Beth Stroupe at Florida State University, we are currently optimizing crystal formation conditions for Dbp6. Using a real-time fluorescence based helicase activity, we have also investigated the RNA unwinding activity of Dbp6. While Ded1, a well-characterized DEAD-box protein, unwinds the RNA duplex, Dbp6 appears to have no unwinding activity. Future directions include adding known protein binding partners of Dbp6 in the RNA duplex unwinding assay and also characterizing its ATPase activity.

Currently, a promising condition for crystal formation involves the addition of fluoride salts and polyethylene glycol. Solving the crystal structure of Dbp6 will aid in elucidating its molecular mechanism. Dbp6 has a human ortholog, DDX51, and the upregulation of this protein

in humans has been associated with the proliferation of non-small cell lung cancer. The findings from this research will therefore aid in translational research, spreading knowledge and information to fields such as pharmacology to develop DDX51 drug targets based on the understandings of Dbp6 found through the basic scientific research completed in this project.

BBB P32 - **The Effects of Synthetic and Natural Compounds on Beta Amyloid Induced Neurodegeneration and Survival in a *C. elegans* Alzheimer's Model**

Zoe Burch[1], Claire O'Connor[2]

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More than 5 million Americans over the age of 65 suffer with loss of memory, independence and bodily function due to the ravages of Alzheimer's Disease. Three major pathologies are noted in the brains of Alzheimer's patients: beta amyloid plaques, neurofibrillary tangles and inflammation. This study utilizes specific synthetic and natural compounds to investigate their possible neuroprotective effects on an Alzheimer's Disease (AD) model containing beta amyloid plaque pathology in *Caenorhabditis elegans.* Neuroprotection was determined by the presence of sustained green fluorescence in the animal's caudal glutamatergic neurons as the animal aged. Here we show that a statistically significant neuroprotection from plaque-associated neurodegeneration in *C. elegans* occurs when treatment with the test compounds is in place during adulthood. To determine if the neuroprotection translates to an increase in survival, longevity studies were also conducted.

BBB P33 - Prevalence of *Cryptosporidium* and Salmonella in *Branta Canadasis* in the Southeastern U.S

Liberty Sheppard

Emory & Henry College, Emory, VA

Birds are known to serve as mechanical vectors for a variety of microorganisms that are infectious to humans. Canada geese (*Branta canadensis*) are migratory waterfowl that are known to vector of variety of pathogens capable of infecting humans by passing them into the environment through their feces. Due to the increase of Canada Geese populations in recreational and residential areas, there is also an increased risk for humans to become infected with the pathogens they carry. This research investigates the presence of Salmonella, *Cryptosporidium*, and other parasitic protozoa. in fecal samples collected from Canada Geese found in North Carolina, Tennessee, and Virginia. A total of 124 samples from seven different localities were tested for presence of Salmonella and *Cryptosporidium*. Of the 124 fecal samples tested, 89 (= 71.8%) were positive for Salmonella, 24 (=22%) were positive for *Cryptosporidium*, and 19 (=15.3%) were positive for both. As many species of Salmonella and *Cryptosporidium* are zoonotic pathogens, these data indicate a potential public health hazard where human-animal (fecal) contact is possible.

BBB P34 - The Effects of Gibberellic Acid on Strawberry Plant Growth

Abriana Lawson

Emory & Henry College, Emory, VA

Gibberellic Acid (GA) is a plant growth regulator, and a model molecule for chemically altering plants. GA is known for promoting growth in a variety of plants, physiologically, developmentally, and in response to environmental stimuli and stressors. In regards to experiments treating strawberry plants with GA, there is not much literature. Foliar sprays of GA in strawberry plants have shown to greatly increase vegetative characteristics, as well as flowering, overall yield, and more. There is less information available about the optimal GA treatment strategy in strawberries. My project aims to bridge that gap, testing aqueous GA treatment rather than a foliar spray. I collected data on vegetative growth and fruit yield with a particular interest in berry size. The first trial of my experiment showed that the GA treatment influenced the vegetative stems and the overall size of the plant by very visible qualitative differences. Many more berries came from the treated plants, however they were overall smaller with very unusual morphology. The GA may have caused a shift in resources to the vegetative growth, rather than promoting berry growth in the plants. Future research could test the effects of inhibiting GA in strawberry plants; this may direct the plants' energy into promoting the berry size and direct less energy into the vegetation. The second trial of my experiment is currently in progress but is starting to show similar results.

BBB P35 - Mortal Kombat: Predicting Colony Recognition in Southeastern Argentine Ant Colonies

Katherine Barrs

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Chemical graph theory is a quickly growing interdisciplinary field involving the graphical analysis of chemical compounds through their molecular structure. Chemical indices are a way of describing and assigning a numerical value to chemical structures which often correlates with the chemical's properties. In this study, we propose the development of a chemical index to predict the behavioral response in a biological system. Argentine ants, *Linepithema humile*, are a globally invasive species that displaces native species and facilitates agricultural pests. Colonies occupy distinct territories and defend them against other colonies. Ants have a waxy coating of cuticular hydrocarbons (CHCs) and can detect (i.e. smell) differences in these CHCs to identify their own vs foreign colonies. In the US, Argentine ants are found across California but only form four massive colonies showing mutual aggression, some spanning more than 500 miles. In the Southeast, we have identified several smaller colonies based on behavioral differences across lesser distances. It is currently unknown why the California ants form a single colony across such distances while the Southeastern ants are found in many smaller colonies. The CHC profiles of the four colonies in California are known to contain over 70 chemicals, but it is unclear which components are most important for recognition. Using previously collected data, we plan to analyze the known chemical components of CHC profiles. Then, we will define a chemical index to apply to chemical structures to predict colony recognition in previously untested colonies. Overall,

better understanding of the differences between California and Southeastern colonies may be key to stopping the spread of these highly invasive insects.

BBB P36 - The Effects of Tetracycline on the Expression of Cyclin Dependent Kinase 1 and Cyclin B in Rotifers

Malarie Schexnider

Erskine College, Due West, SC

The overuse use of antibiotics has become an increasing problem. Specifically, the excessive use of tetracycline in agriculture has increased the environmental levels of antibiotics. Antibiotic runoff has become a prevalent issue because of the negative effects on aquatic life, such as the microscopic, invertebrate rotifer. In our previous study, rotifers from the species *Philodina acuticornis* were exposed to varying environmental concentrations of tetracycline. The results of this study showed that rotifers exposed to higher concentrations of tetracycline saw a delay in egg production. In this study, a possible mechanism for this delay is examined through the effects of tetracycline on the expression of cyclin B and cyclin dependent kinase 1, which control the activation of the egg maturation pathway. Rotifers that are exposed to environmental levels of tetracycline will show decreased expression of cyclin dependent kinase 1, indicating that the egg maturation process is not being activated. *Philodina acuticornis* rotifers were exposed to 25 mg/L of tetracycline for 1 week. Expression was assessed through total RNA isolation and cDNA synthesis of the cyclin B and cyclin dependent kinase 1 genes. The results of this study are inconclusive because the expression of cyclin B and cyclin dependent kinase 1 could not be measured, as the available rotifer DNA sequences were not conserved between the *Philodina acuticornis* and *Brachionus calyciflorus* rotifer species.

BBB P37 - Identification of transcription factor complexes from ENCODE IP-Mass spec data

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Transcription factors (TFs) are proteins involved in the regulation of transcription and are essential for the expression of genes. Generally, transcription factors form complexes to accomplish that. Immunoprecipitation is a technique used to isolate a protein of interest, and mass spectrometry is used to determine the compounds in a sample. By performing immunoprecipitation followed by mass spectrometry (IP-MS) on a known TF, the factors interacting with the assayed TF can be identified. The files analyzed for this project were the results from performing these two techniques on a known TF. The files analyzed represent IP-MS data collected over a 5-year period for protein validation of ENCODE ChIP-seq datasets. As this data has already served its originally intended purpose, TF complex identification presents a new use case for these already-existing assay data files. After analysis of IP-MS data for known transcription factors' interactions, some known and unknown complexes were observed. This information adds to the still-growing knowledge on transcription factor complexes and their role in gene regulation.

BBB P38 - Bird Seed and Bird Feeder Interactions at Midway University: A Continued Study

Rachelle Felski

Midway University, Midway, KY

Below Midway University campus, next to the Lee Branch Stream are three areas: woodland, ecotone, and park-like grassland. Research conducted in the fall of 2019 was in the ecotone, the interface between the woodland and park-like grassland. Research was done to increase primary empirical data on group and individual bird seed selections. This was done by looking at both aggregate and individual selection for bird feeder/bird seed types. A list was also developed of the birds populating the area. This study used three types of bird seed: white proso millet, safflower, and black-oil sunflower, as well as three different feeder types: hopper, platform, and tube. Three different combinations (1, 2, and 3) were developed so that each feeder, with appropriate seed type, was hung on a three-armed pole for two weeks. Criteria for selection was a bird perch visit, with feeding occurring. Observation period was from 0700 to 1000 hours and continued until 90 hours were met. For combination 1, there was an aggregate selection for platform/safflower, followed by tube/black-oil sunflower, and lastly hopper/white proso millet; with six substantial contributions to an association. For combination 2, there was an aggregate selection for tube/safflower, followed by hopper/black-oil sunflower, and lastly platform/white proso millet; with six substantial contributions to an association. For combination 3, there was an aggregate selection for hopper/safflower, followed by platform/black-oil sunflower, and lastly tube/white proso millet; with three substantial contributions to an association. There was a total of 11 species of bird populating the area. Overall, it appears there was interspecific and intraspecific competition influencing both aggregate and individual bird selections for each combination. It appears that birds may have tracked certain seed type regardless of feeder type. This may have occurred because of seed nutrition.

BBB P39 - Arboreal Epiphytes in the Soil-Atmosphere Interface: How Often Are the Biggest "Buckets" in the Canopy Empty?

Hailey Hargis

Georgia Southern University Undergraduate Student, Statesboro, GA

Abstract: Arboreal epiphytes (plants residing in forest canopies) are present across all major climate zones and play important roles in forest biogeochemistry. The substantial water storage capacity per unit area of the epiphyte "bucket" is a key attribute underlying their capability to influence forest hydrological processes and their related mass and energy flows. It is commonly assumed that the epiphyte bucket remains saturated, or near-saturated, most of the time; thus, epiphytes (particularly vascular epiphytes) can store little precipitation, limiting their impact on the forest canopy water budget. We present evidence that contradicts this common assumption from (i) an examination of past research; (ii) new datasets on vascular epiphyte and epi-soil water relations at a tropical montane cloud forest (Monteverde, Costa Rica); and (iii) a glob-

al evaluation of non-vascular epiphyte saturation state using a process-based vegetation model, LiBry. All analyses found that the external and internal water storage capacity of epiphyte communities is highly dynamic and frequently available to intercept precipitation. Globally, non-vascular epiphytes spend <20% of their time near saturation and regionally, including the humid tropics, model results found that non-vascular epiphytes spend ~1/3 of their time in the dry state (0–10% of water storage capacity). Even data from Costa Rican cloud forest sites found the epiphyte community was saturated only 1/3 of the time and that internal leaf water storage was temporally dynamic enough to aid in precipitation interception. Analysis of the epi-soils associated with epiphytes further revealed the extent to which the epiphyte bucket emptied—as even the canopy soils were often <50% saturated (29–53% of all days observed). Results clearly show that the epiphyte bucket is more dynamic than currently assumed, meriting further research on epiphyte roles in precipitation interception, redistribution to the surface and chemical composition of "net" precipitation waters reaching the surface.

BBB P40 - Small Mammal Richness and Abundance in the Walter Bradley Park, Midway, KY USA

Larissa Cussins

Midway University, Midway, KY

Small mammals provide ecosystem services in the environments they live in. They benefit humans, animals, and plants in the community. This study was designed to investigate small mammal richness with a focus on diversity in the Walter Bradley Park, Midway, KY USA. The study branched off from a previous study conducted on Midway University's Campus, Midway, KY USA done by a former student, Raven Cannon, in June of 2018. Performed in the Fall of 2019 this study focused on three different habitat types: riparian, grassland, and ecotone in which 13 species of small mammals presumably reside. Each habitat type was sampled for vegetation, in which the grassland experienced the most ground coverage and least canopy cover; the riparian areas experienced the least ground cover and the most canopy cover; canopy and ground coverage was intermediate in the ecotone habitat. Methods included Sherman live traps, which were used for temporary capture followed by release of small mammals. There was a total of eight captures out of 140 trap nights. Three species were captured: *Blarina brevicauda, Peromyscus maniculatus, Peromyscus leucopus.* Small mammals were primarily found in the grasslands and riparian areas; no animals were captured in ecotone habitats. Number of captures was too small to determine diversity, which was a limitation also seen in the work done by Cannon the previous year.

BBB P41 - The Comparison of P. aeruginosa Found in Residential and Pasture-land in Central Kentucky

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Pseudomonas aeruginosa is considered one of the most prevalent bacteria in human and animal infections. The origin of this bacterium and how it is passed on to humans and animals is varied. However, evidence suggests that soil can play a major role in transmission of P. aeruginosa. In this study, soil samples were collected from pasture-land and residential land from farms in Central Kentucky in paired samples. A total of 18 samples of soil were gathered and grown on Pseudomonas Isolation Agar to select for pseudomonads and related species. In addition, PCR analysis of 16S rDNA and rpoD regions were conducted to determine which colonies were Pseudomonas species and to detect any Pseudomonas aeruginosa strains. Nineteen colonies were gathered from pasture-land and twenty-nine colonies were gathered from residential land. To date, at least seven of these colonies are confirmed to be from the genus Pseudomonas. Though research is still currently being conducted, it can be said that Pseudomonas species have been detected in the soil of Central Kentucky.

BBB P42 - Effects of a Chicken Processing Plant on Locust Fork Watershed in Blount County, Alabama

Elizabeth Harris

Samford University, Birmingham, AL

There are 3,000 chicken processing plants in the United States. Chicken fecal matter contains high concentrations of nitrates, which can cause central nervous disorders in adults and "blue baby syndrome" in infants under 6 months old (Water Quality Association, 2014). A large chicken processing plant in Blount County, AL releases waste water into Graves Creek, a tributary of the Locust Fork of the Black Warrior River; both waterways have recreational and residential use. To assess the impact of this processing plant, grab samples were collected 4 times from 8 different sites in Graves Creek and the Locust Fork over the course of 8 months. Conductivity was measured on site and each water sample was subsequently tested for nitrates. In Graves Creek, mean conductivity and mean nitrates were significantly greater downstream from a wetland input coming from the plant than upstream. In addition, mean conductivity and mean nitrates in the Locust Fork were significantly greater downstream from the mouth of Graves Creek than upstream. The maximum ideal conductivity for freshwater streams is 500 µS/cm (EPA, 2012) and the maximum safe nitrate concentration in waterways is 44.2 mg/L (Water Quality Association, 2014). Mean conductivity and nitrates in Graves Creek were above the maximum ideal concentrations for each of the downstream locations, suggesting that the water coming from the plant poses a threat to aquatic life in Graves Creek and to the surrounding community.

BBB P43 - Tracking Movement of a Federally Threatened Mussel, *Fusconaia escambia*, During the Drawdown of Gantt Reservoir

Nguyen Tien Anh Quach, Meet Patel

Troy University, Troy, AL

Droughts have become more prevalent in the southeastern region of the US and are anticipated to be more common in the future. Such conditions adversely impact aquatic organisms with limited mobility, including mussels. This study was performed to determine if *Fusconaia escambia* (Narrow pigtoe, federally threatened) and *Elliptio pullata* (Gulf spike, common species) tracked the receding water and/

or burrowed in response to the drawdown of Gantt Reservoir in fall 2019, and if differences existed between species. Eleven individuals of each species were collected two weeks prior to the drawdown and uniquely tagged using Biomark PIT tags and a 10-cm monofilament line to determine burrowing depth. Mussels were placed parallel to the bank at 0.6 m depth and spaced about one meter apart. Approximately two weeks after the drawdown initiated, linear distance traveled for each individual was measured. Results showed that 55% of *F. escambia* and 64% of *E. pullata* responded to the event by burrowing into the substrate. Shell length was shown to be significantly negatively correlated with movement for *F. escambia* ($r = -0.77$, $p = 0.005$). In addition, there was no measurable deviation from downhill movement, which was likely due to the direction of receding water and absence of flow. No significant difference in linear distance traveled were found between species ($p = 0.24$). This study suggested that mussels moved in a downhill direction tracking the receding water rather than showing variation or random movement. Under drought stream conditions, where water levels typically recede at a slower rate, many individuals may have been able to track the receding water and survive. Due to limited number of federally threatened *F. escambia* available, further studies are needed to precisely describe and quantify differing movement variables, which would be helpful in the preservation of freshwater fauna of the Southeastern US.

BBB P44 - Freshwater Mussel Survivability Over The 13 Week Drawdown of Gantt Reservoir

Meet Patel, Nguyen Tien Anh Quach

Troy University, Troy, AL

Alabama is known as the most diverse state in North America for freshwater mussels with more than 180 documented species, although 27 are extinct, 22 are extirpated from the state, and 39 species are federally threatened or endangered. The largest known population of *Fusconaia escambia*, a federally threatened species, was known to occur in Gantt Reservoir in southeast Alabama. A planned 13-week reservoir drawdown occurred in fall 2019 for routine dam maintenance and initiated a study on mussels to determine survival time, in addition to revealing other variables that may play a role in survivability. Sampling occurred weekly and included excavation of 24 - ¼ m^2 quadrats to 15 cm depth. Soil temperature and moisture were measured for each sample at 10 cm depths, and substrate composition, cover, and lakebed depth were recorded. All live and fresh dead mussels collected were identified and measured. *Elliptio pullata* accounted for 87% of all mussels collected and >99% of live individuals. Of the total *E. pullata* collected (n = 875), 16% were found live beneath the surface while 8% were found live and exposed at the surface. Results indicated that various types of cover over the substrate contributed to survival with an average of 54% survival of *E. pullata* at locations with cover (natural or anthropogenically derived) compared to 18% live with only substrates present. Although only one live specimen of *F. escambia* was found (week 2), *E. pullata* was found to survive the duration of the drawdown. Furthermore, 68% of *F. escambia* collected were found between 2-3 m depths, meanwhile 69% of *E. pullata* were found at ≤1 m depth, indicating variations in habitat preferences. More in depth analyses of the data will be directed towards if survival was related to substrate type, moisture, temperature, or other variables recorded throughout the drawdown.

BBB P45 - Survey of Pathogenic Bacteria in Mobile and Bon Secour Bays

Nisha Bista, Shraddha ChandThakuri, Anushka KC

Troy University, Troy, AL

This research is designed to detect diverse waterborne bacterial pathogens in Mobile and Bon Secour Bays (Mobile, AL). The ultimate goal of this research is to assess the risk to public health by understanding types of waterborne pathogens. In order to achieve the goal, we hypothesized that potentially pathogenic bacteria exist in Mobile and Bon Secour Bays. This hypothesis will be examined by detecting and identifying 15 genera of pathogenic bacteria in sediment samples collected from five sampling sites in Mobile and Bon Secour Bays.

BBB P46 - Antibiotic Resistant Enterococci in 'No Antibiotics Ever' Poultry Products

Micayla Shirley

Georgia Southern University, Statesboro, GA; Beta Beta Beta Biological Honor Society Tau Kappa Chapter, Statesboro, GA; United States Department of Agriculture, Athens, GA

Poultry products labeled "No Antibiotics Ever (NAE)" have become popular as concerns have increased over the use of antibiotics in food animals and the potential of antibiotic resistant bacteria transferring into the human population. As previous studies on retail meat have shown the presence of antibiotic-resistant bacteria on those products, this study investigated the presence of the antibiotic-resistant enterococci on NAE poultry products. During the summer of 2019, 10 poultry products designated as NAE were purchased from grocery stores in the Athens, Georgia area and cultured for the presence of enterococci. Presumptive enterococcal isolates were identified to genus and species and then analyzed for antibiotic susceptibility to a panel of 15 antibiotics. All (100%) chicken (boneless skinless chicken breasts, breast strips, and thighs; chicken drumsticks, liver and wings; white meat ground chicken) and turkey samples (ground turkey) were positive for enterococci. The predominant species from all products was *Enterococcus faecalis* (n=24), while an unidentified species of *Enterococcus spp.* (n=2) was isolated from chicken drumsticks and white meat ground chicken. Approximately 87.5% (21/24) of *E. faecalis* were resistant to lincomycin, followed by 62.5% (15/24) to tetracycline. Although 79.2% of *E. faecalis* were resistant to the human medical use drug, Synercid, this was attributed to intrinsic resistance of *E. faecalis* to this antimicrobial. Resistance to other human medical use antibiotics, tigecycline (41.7%) and linezolid (4.2%), was also observed. This data suggests that NAE poultry products are a source of antibiotic-resistant enterococci that can be transferred to humans.

Beta Beta Beta Research Grant Recipients

The National Executive Committee for Beta Beta Beta awarded 145 TriBeta Research Grants for 2019-2020. A total of 193 applications were submitted. The total amount awarded was $75,712.85. Grants ranged from $50 to $1437. This year the students of the Southeast Region received 20 Grants with 10 recipients from SE District I and 10 from SE District 2. The students of the Southeast traditionally are required to present their data at the TriBeta Regional or National Conference, although this year this requirement was waived.

Southeast Region Grant Awardees

Claire Featherstone, Catawba College, Tau Eta, SE-1

Sydney Goertzen and Brooke Freeman, Catawba College, Tau Eta, SE-1

Sarah Emerick, Eckerd College, Kappa Delta Epsilon, SE-1

Sean Janovic, Elon University, Sigma Mu, SE-1

Drew Capuzzi, James Madison University, Psi Beta, SE-1

Hunter A Merrill, Lander University, Psi Theta, SE-1

MaryEllen Haas, Marymount University, Eta Kappa, SE-1

Mary V. Silvestro, Nova Southeastern University, Rho Rho, SE-1

Austin Jaime, Point University, Psi Alpha Psi, SE-1

Irene Kuriakose, Queens University of Charlotte, Tau Tau, SE-1

Abigail Kruger, Columbus State University, Mu Omicron, SE-2

Destiny Sciuva, Columbus State University, Mu Omicron, SE-2

Kyra Drobny and Avery Roland, Lipscomb University, Kappa Delta Alpha, SE-2

Jennie Hibma, Lipscomb University, Kappa Delta Alpha, SE-2

Haley Kling, Lipscomb University, Kappa Delta Alpha, SE-2

Theodore Reed, Lipscomb University, Kappa Delta Alpha, SE-2

Nisha Bista, Joseph Blake Dawkins, Shraddha Chand Thakuri, and K C Anushka, Troy University, Mu Epsilon, SE-2

Amber Greenburg, Union University, Kappa Alpha Kappa, SE-2

Taylor Lewelling, Union University, Kappa Alpha Kappa, SE-2

Mohammad Hamed, University of New Orleans, Kappa Chi, SE-2

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In Memoriam

Dr. Lafayette Frederick
1923-2018

Dr. Lafayette Frederick was born March 19, 1923 in a small rural town near Friarspoint Mississippi in Coahoma County that had the name "Dog Bog". He was the second child and first son of five children born to the late James D. and Ellen Frederick. Lafayette grew up in Southeast Missouri.

Lafayette's education following high school included Tuskegee Institute (1943), University of Hawaii (1946-1948), University of Rhode Island (1948-1950), and Washington State University (1950-1952). Lafayette was a United States Navy Veteran.

Throughout 65 years, Lafayette taught at Southern University (Baton Rouge, LA), Atlanta University, Visiting Scientist at the University of Georgia, Central State University, Howard University, Cornell University, University of Illinois, and Visiting Scientist at Tuskegee University. Lafayette was responsible for taking many students to professional meetings throughout the United States and abroad as his greatest passion was to assist students in reaching their future goals and move on to their chosen professions.

Among the many awards he has received are: National Science Foundation Scholar, History Makers, AAAS Scholar, Mycological Society, and American Phytopathological Society. Lafayette had a great love for his alma mater, Tuskegee Institute (now Tuskegee University), where he served as local president of several alumni clubs wherever he resided and was President of the National Alumni Association. He was also an Eminent Presidential Associate, and a member of the George Washington Carver Foundation.

Lafayette was very active in church programs, such as boy scouts, Black History Month, Men's prayer breakfast, and jail ministry. His favorite sports were baseball and tennis. Above all, Lafayette was a deeply religious person who had a deep love for his family and people.

On Saturday, December 29, 2018, he entered eternal rest peacefully at his home in Tuskegee, Alabama.

Lafayette leaves to cherish his memories, a loving and devoted wife of 68 years, Antoinette; children Lewis (Melody) Frederick, Karla (Carl) Miller and David Frederick; grandchildren, David Anthony Frederick, Gwynedd Frederick, Carl Lenn (Valencia) Miller, Sharece (Michael) Curry, Paul (Aftan) Miller, Stephan Miller, Leah Miller, Anthony Miller, Lara Miller, and Kayla Moriah Miller; great grandchildren Paul Lafayette Miller, Paige Miller, Preston Miller, Lina Miller, Layla Miller, Lia Miller, and Vivianne Miller; sisters Dorothy Frederick Walker and Irma Frederick Kendrick; adopted children John and Annie L. Brown, and a host of nieces, nephews, friends, former colleagues, and students.

Dr. Frederick's obituary was printed for his memorial service and was shared by his student, Chinyere Knight. Photo credit: Jason Varney Photography.

In Memoriam

Mrs. Antoinette Arlene Marie Reed Frederick
1929-2020

Each day was an adventure for Antoinette Arlene Marie Reed Frederick. Sometimes the adventure was simply finding a new friend to talk to at the store or in church, hearing the new story and the hopes of a Tuskegee choir student. At other times, she was heading off to Australia, The Great Wall of China, or a cruise along the Alaskan coast. She always had two bags packed and ready to go. Nothing in her early life in Rhode Island could have foretold the world traveler that she became or the hundreds of people who became adopted family to her children David, Karla, and Lewis. Yet the seeds for a life of adventure were there, long before she married Lafayette (Fred) Frederick.

Ann was born May 15 in 1929 in Providence, Rhode Island. She married Lafayette Frederick in 1950 and moved to Pullman, Washington. Son, Lew Frederick, was born there. They moved back to Rhode Island for a short time. Then to Scotlandville, Louisiana where Fred became a Biology professor at Southern University. Daughter, Karla, and son, David arrived shortly after that.
She began a life long mission of feeding and supporting hundreds of college students and others including the many Tuskegee Alumni and Fred's classmates, the Tuskegee Airmen. Her skills as a secretary made her an invaluable support for academic, ecclesiastical and military offices. Her determination sustained her as the family became deeply involved in the Civil Rights movements of the 1950's and 1960's. She took on roles in a range of volunteer groups ranging from church choirs, the boy scouts, to hospital greeter. Her most recent and rewarding time was been spent as the chaperone for the Tuskegee University Choir.

It will be impossible to list all of the people she affected during her long life. Immediate Family members include: Children (spouses)-Karla (Carl), David, Lewis (Melody). Grandchildren- Carl Lenn (Valencia), Sharece Ann (Michael), Paul Lafayette (Aftan), Lara, Stephen, Leah, Anthony, Kayla Mariah, Gwynedd, David (Jenny). Nine Great Grand Children; Sister-in-Laws- Irma, Dorothy; Aunt -Virginia Reed Hamilton; A list of Cousins, Nieces, Nephews and their spouses would be too long to mention here. She had a very Special relationship with Outstanding neighbors-Tuskegee Mayor Pro Tem Annie and John Brown. She was especially fond of the time she spent with First Lady Michelle Obama and Coretta Scott King.

A special thanks to Rev. Dr. Gregory S. Gray and Dr. Elaine Harrington, Tuskegee University President Lily McNair, Tuskegee Choir director, Dr. Wayne Barr and the entire Tuskegee University faculty and Alumni, the friendly and supportive Tuskegee neighbors and community, and Tuskegee Mayor Lawrence "Tony" Haygood, Jr.

Ann's husband, Lafayette Frederick passed away in December 2018. They were quite a team. As one friend said: "Their deep faith surrounded them. They did not just Go to church, they became the church. It was not just words, it was actions."

For Ann, it was a sense of joy in the adventure of life.

Mrs. Frederick's obituary was prepared by her son, Lew Frederick, and shared by her son, David Frederick.

In Memoriam

Dr. Joe Everett Winstead
1938-2019

Joe Everett Winstead was born in Wichita Falls, Texas to Leonard E. Winstead and Nellie Helen (Reaser) Winstead on March 17, 1938. Thanks to the quick actions of his mother, the deal his older sister, Janet, made to trade her baby brother to a neighbor for a puppy fell through – much to Janet's chagrin! Joe went on to grow up doing all the things a kid in north Texas might do - riding horses, hanging out at the local drug store, and delivering telegrams during WW2. After high school he embarked on his journey through higher education which never really ended. Following Janet to Midwestern State University, Joe was mentored by Dr. Art Beyer who was not only a teacher but also employed Joe on the grounds "Crew" which, when not chasing jack rabbits on bush hogs, did its best to beautify the campus. Joe played clarinet in the Midwestern band and was a performer in the band's Cavalcade of Melody shows (which may explain in part his daughters' careers in the performing arts and not the sciences!). Joe then earned his MS at Ohio University, served as a captain in the US Army, and survived (literally & figuratively) the PhD program at the University of Texas.

After many years on the faculty of Western Kentucky University, Joe ventured into the dark side of academia by becoming the chair of the department of biology at Morehead State University. His fate was sealed when he was offered the position of Dean of the College of Science and Technology at Arkansas Southern University. When not annoying upper administration on behalf of his students and faculty, Joe served terms as president of the Kentucky Academy of Science, Southern Appalachian Botanical Society and the Association of Southeastern Biologists and endeavored to enlighten the creationists and climate change deniers of the world. After retirement, Joe returned to the light by traveling, doing consulting work, research projects, enjoying fine scotch whiskey, and spoiling his dogs. Joe went that "big rodeo in the sky" on November 20, 2019.

Preceding him in death are sisters, Janet and Martha. Joe is survived by his pesky little brother, Leonard (Butch) Winstead of Newscastle, Texas; daughters Cynthia Backstrom-Winstead (Håkan) of Springfield, Missouri; Courtney Cunningham (Dustin) of Orlando, Florida; wife Jessie L. Wren of Westview, Kentucky; devoted step children and a menagerie of grandchildren and great grandchildren.

In lieu of a funeral, Joe requests that you visit your local Waffle House or Huddle House restaurant and have a piece of pie and a cup of coffee in his honor. He also requests that you vote early and often! If you don't like pie, a donation to Hosparus Kentucky would be appreciated.

Dr. Winstead's obituary was shared by Dr. Michael Held.

In Memoriam

Dr. Edward Ernst Cooper Clebsch
1929-2019

As snow blanketed the Smokies, Edward (Ed) Ernst Cooper Clebsch (June 6, 1929 – December 14, 2019) passed away in peace surrounded by his family.

He was born in Clarksville, Tennessee to Julia (Wilee) and Alfred Bernhard Clebsch, an immigrant from Bremen, Germany. Dr. Edward Clebsch, Professor Emeritus spent most of his life living in Tennessee: Clarksville, Knoxville, Greenback, Norris, and Oak Ridge.

His father instilled in him a deep love of the natural world and music. Memories of his fun-loving mother's cooking inspired him to become a consummate bread baker. Ed was always happy to share a loaf with friends.

He was a Clarksville High School graduate (1947), then played piccolo and flute in the Army band during the Korean War (1951-1952). At fourteen, Ed knew he wanted to be a botanist. He earned his bachelor's (1947-50, 1953-55) and master's degrees in Botany (1955-57) at the University of Tennessee, Knoxville. His PhD (1957-60) was earned at Duke University with a dissertation on Tristetum spicatum in far northern Alaska.

Dr. Ed Clebsch, PhD became a Botany professor at the University of Tennessee Knoxville in 1963 and played a leadership role in developing the UT program in ecological sciences. His research took him to many places, including Alaska, Montana, Idaho, and Great Smoky Mountains National Park.As a gifted professor and lifelong ponderer of the wonders of the world, Ed influenced many lives: his love of plants, innate understanding of ecology, outdoor skills, and great sense of humor motivated many students to pursue careers in the natural sciences. He advised 32 MS, 17 PhD, as well as two postdoctoral fellows in the ecology of tundra, catfish, earthworms, biogeochemistry, biogeography, and plant populations.

He co-wrote and supervised more than 100 scientific publications (40 as primary author), theses, and dissertations. Participating and belonging to over 60 organizations and committees during his 90 years, he was instrumental in the creation of many lasting endeavors, including the Spring Wildflower Pilgrimage, the UTK Arboretum, Smoky Mountains Field School, and Tennessee Citizens for Wilderness Planning. Dr. Clebsch was sought after as a presenter and field trip leader outside of academia. He was the recipient of a Community Outreach Service Award in the College of Liberal Arts of the University of Tennessee in 1990 for his public service. On the river, up a mountain, and around the campfire, Ed transferred his curiosity and excitement to his students, earning him the Meritorious Teaching Award of the Association of Southeastern Biologists in 1998, among other career awards. Being a lifelong voracious reader, he belonged to a book club in Oak Ridge known for its lively discussions, good food, and deep friendships.

Dr. Edward E. C. Clebsch will be missed and has left a legacy of love and laughter.
He leaves 3 children, Liese Clebsch Dean (Idaho), Julia Clebsch (West Virginia), Hans Clebsch (Ohio), their spouses, and his two grandchildren, Luis C. Clebsch and Cooper D. Dean. He was preceded in death by his two older brothers Alfred and William Clebsch. Following in the footsteps of his passions, his daughters worked for the US Forest Service and the National Park Service, and his son plays French Horn with the Cleveland Orchestra.

There will be no memorial service, but following Ed's wishes, a celebration of his life is in the planning.
In lieu of flowers, the family requests that donations be made in his memory to Tennessee Citizens for Wilderness Planning, TCWP, P. O. Box 6873, Oak Ridge, Tennessee 37830.

Dr. Clebsch's obituary was prepared by Julia Clebsch, Liese Clebsch Dean, and Hans Clebsch.

The *Southeastern Naturalist* and *EBio* are the official journals of ASB.

Together, they serve as research and publishing resources that cover the full spectrum of subject matter interests of members of ASB.

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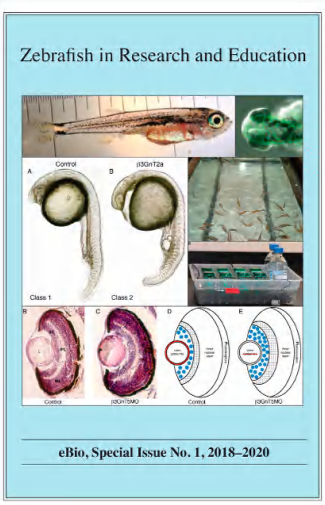

PATRON MEMBER

Mike Dennis
Breedlove, Dennis, & Associates, Inc. (BDA)
Winter Park, Florida

Patron membership is for individuals who choose to support the society beyond annual meeting registration costs. Patron membership includes a one-year membership, one annual meeting registration and two tickets to each of the three evening events at the annual meeting (the Plenary Mixer, the Social, and the Awards Banquet). ASB Patron members choosing to receive SENA must pay $20 per year for the SENA subscription, which is a $35 per year discount over non-ASB member subscription rates.

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